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**Patentanmeldung Nr.    Patent application No.    Demande de brevet n°**

04290818.6

Der Präsident des Europäischen Patentamts;  
Im Auftrag

For the President of the European Patent Office

Le Président de l'Office européen des brevets  
p.o.

**R C van Dijk**





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Mutabilis SA  
156, Avenue Vaugirard  
75730 Paris Cedex 15  
FRANCE

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If no title is shown please refer to the description.  
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Compositions of polypeptides specific to pathogenic strains and their use as  
vaccines and in immunotherapy

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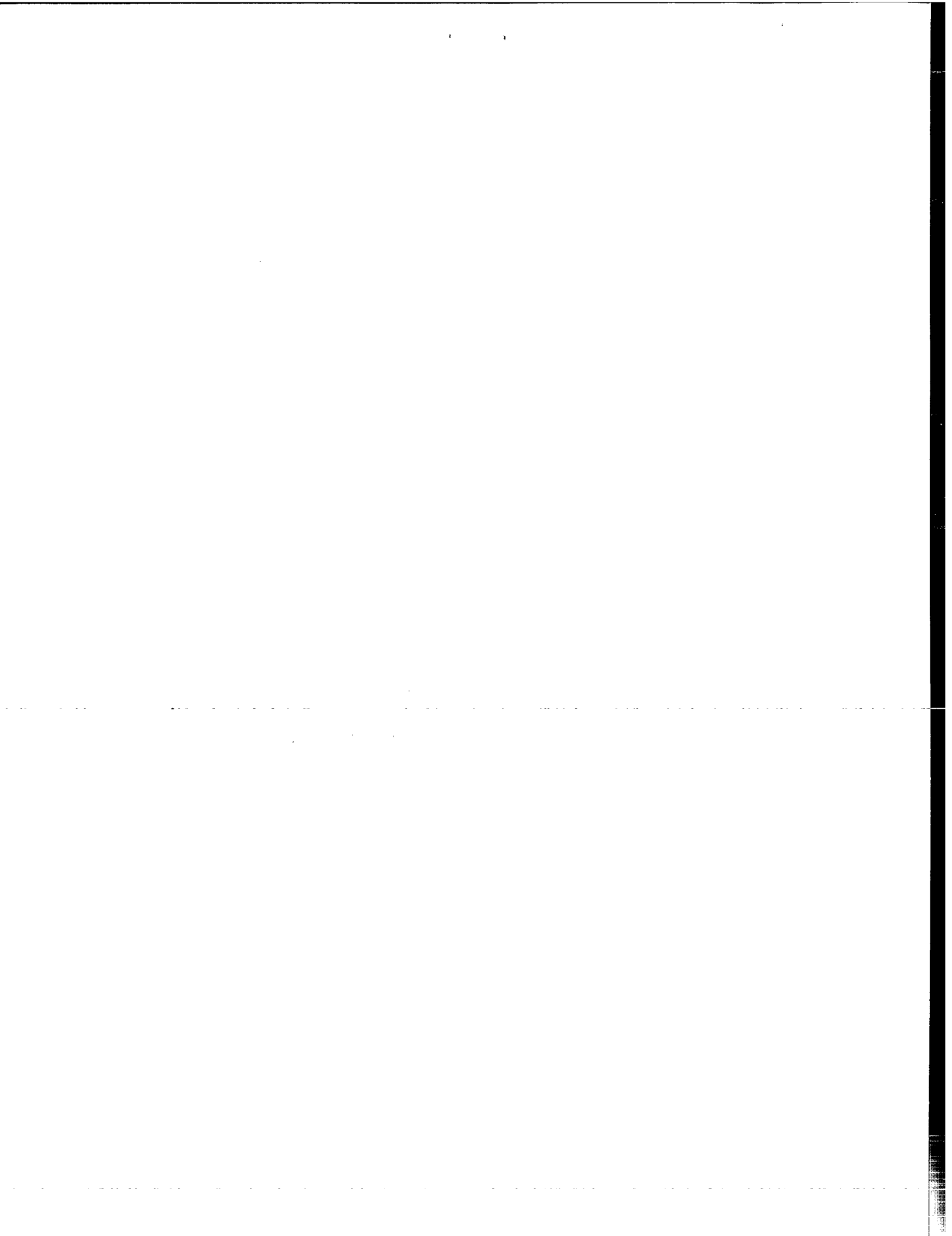
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**"Compositions of polypeptides specific to pathogenic strains  
and their use as vaccines and in immunotherapy "**

The invention relates to new compositions of polypeptides specific to pathogenic strains, particularly to extra-intestinal *E. coli* strains.

- 5 It more particularly relates to combinations of antigenic polypeptides and combinations of antibodies directed against said polypeptides and to their use as vaccines and in immunotherapy, respectively.
- 10 Although *Escherichia coli* is probably the best known bacterial species and is one of the most common isolated in clinical microbiology laboratories, misconceptions abound regarding the various types of *E. coli* and the infections they cause.
- 15 *E. coli* strains of biological significance to humans can be broadly classified in 3 major groups:
  1. Commensal strains, which are part of the normal flora.
  2. Intestinal pathogenic strains, which are not part of the normal flora. This group contains various pathotypes (EPEC, EHEC, ETEC, EIEC) not including *Shigella*.
  - 20 3. Extra-intestinal strains (ExPEC) which are responsible for infections outside the gastro-intestinal (GI) tract, but can also be part of the normal flora. All hosts, either immunocompromised or not are susceptible to these infections.
- 25 ExPEC strains are responsible for the majority of the urinary tract infections (UTI) particularly cystitis, pyelonephritis, and catheter associated infections.
- 30 They are also responsible for abdominal infections, nosocomial pneumoniae, neonatal meningitidis, soft tissue infections, and

bone infections. Each one of these localizations can lead to bacteremia with a risk of sepsis in case of organ failure. ExPEC strains are indeed the most common Gram negative bacilli isolated from blood cultures.

5

750 000 cases of bacterial sepsis occur each year in the US, and are responsible for 225 000 deaths. In a recent study on 1690 cases of sepsis, it was shown that the main bacteria species identified is ExPEC (16% of the cases) and then *S.aureus* (14% of the cases).

10

These numbers demonstrate the importance of ExPEC strains in both hospital and community acquired infections.

15 ExPEC strains correspond to a homogenous subset of *E. coli* strains. Analysis of phylogenetic relationships among *E. coli* strains by MLEE has revealed that *E. coli* belong to 4 main phylogenetic groups designated A, B1, B2 and D.

20 The pathogenesis of ExPEC strains is that of extra-cellular microorganisms, i.e., they are well adapted to growth in the extra-cellular fluids and efficiently resist phagocytosis by polymorphonuclear. Initial studies have shown that virulence factors known to be important for the extra-cellular growth are mainly found in B2/D *E. coli.*, thus suggesting that B2/D subgroups contain most of the ExPEC strains. This was reinforced by experiments performed on animals showing that B2/D strains are more virulent than A and B1 strains. Subsequent epidemiological studies have indeed confirmed these hypotheses. B2/D isolates are those predominantly responsible for neonatal meningitidis (87%) and community or nosocomial acquired urosepsis, (93 % and 85%, respectively).

30

Similar results have been reported for cystitis (70% are due to the sole B2 *E. coli*), thus demonstrating that the importance of ExPEC strains.

- 5 These recent findings demonstrate that the B2/D subgroup of strains is the *E. coli* core genome the best adapted to growth in extra-cellular fluids.

10 In addition to this core genome, ExPEC strains have various pathogenicity islands which encode virulence factors associated with the different pathogenesis of extra-intestinal *E. coli* infections (UTI, urosepsis, neonatal meningitidis...). Among the main virulence factors are the capsule, which is well-known to be important for extra-cellular growth, and the  
15 iron chelation systems (aerobactin and enterochelin, for example). In addition, depending on the pathogenesis, these strains can produce toxins (CNF, hemolysin...), adhesins (pap, sfa...) and other iron chelation systems.

- 20 The notion that B2/D *E. coli* correspond to a distinct subset of pathogenic *E. coli* strains is reinforced by the fact that B2/D *E. coli* are not broadly isolated from the stools of humans. They were recovered from only 11% of individuals, whereas A and B1 subgroups are present in the stools of 74% of  
25 the individuals of a human population.

As mentioned above the pathogenesis of ExPEC strains relies on their ability to multiply in the extra-cellular fluids and to resist bactericidal activity of the complement and  
30 phagocytosis by polymorphonuclear. Therefore, as for other extra-cellular pathogens (*Haemophilus influenzae*, *Streptococcus pneumoniae* and *Neisseria meningitidis*) a protective antigen against ExPEC has to induce antibodies

that promote opsonisation and/or the bactericidal activity of serum.

Considering the above statements, an efficient antigen has to  
5 be largely represented among the population of B2/D *E. coli*.

Similarly to other extra-cellular pathogens, the capsular polysaccharide would be an ideal antigen, however most pathogenic B2 strains express the K1 polysaccharide. The  
10 latter has a structure identical to that of group B meningococcus, which is non-immunogenic and shares common antigens with the brain. Another possible target may be the lipopolysaccharide (LPS). However there are a large number of different LPS serotypes that are shared by various subgroups.

15 The inventors have now found that some specific compositions of polypeptides coded by the B2/D genome, but absent from A and B1 *E. coli* strains, are particularly useful as antigens and can specifically prevent the pathologies due to ExPEC  
20 strains. Homologs of these antigenic components can be found in other pathogenic bacterial species and therefore are useful to prevent the pathologies caused by these bacteria. Accordingly, any reference to products specific to ExPEC strains and to their uses will encompass components in these  
25 species.

For example homologous antigens could be present in the following species and be as such used for prevention of disease due to the bacteria:

30 *Pseudomonas aeruginosa*, *Escherichia coli* O157:H7, *Yersinia pestis*, *Vibrio cholerae*, *Legionella pneumophila*, *Salmonella enterica*, *Salmonella typhimurium*, *Haemophilus influenzae*, *Neisseria meningitidis*, *Neisseria gonorrhoeae*,

*Bacillus anthracis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*,  
5 *Helicobacter pylori*, *Klebsiella pneumoniae*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Pseudomonas aeruginosa*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Moxarella catarrhalis*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella*  
10 *sonnei*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, and any species falling within the genera of any of the above species.

It is then an object of the invention to provide new  
15 combinations of isolated antigenic polypeptides, and new combinations of isolated polynucleotides belonging to the core B2/D genome and not present in commensal *E. coli*.

Another object of the invention is to provide new combinations  
20 of antibodies raised against the antigenic polypeptides of said combinations, or peptidic fragments thereof.

It is still another object of the invention to provide vectors  
and host cells containing said polynucleotides.

25 Another object of the invention is to provide vaccine compositions specific to extra intestinal infections caused by ExPEC and pathologies caused by other pathogenic strains expressing antigenic polypeptides homologous to the ExPEC  
30 antigenic polypeptides.

The invention also relates to means for detecting and treating a development of *E. coli* in a human or animal compartment which is extra-intestinal (systemic and non-diarrhoeal

infections, such as septicaemia, pyelonephritis, or meningitis in the newborn).

The combinations of isolated antigenic polypeptides used according to the invention are selected among polypeptides specific to B2/D *E. coli* strains and not present in A and B1 isolates of *E. coli*. They are encoded by genes belonging to the core B2/D genome and are not present in commensal *E. coli*.

- 10 They comprise at least one polypeptide of a first group, having a sequence selected in the group comprising the sequences of SEQ ID N°1 to N°66 or 133-145 and at least one peptide of a second group, having SEQ ID N° 159, or homologous sequences of polypeptides of the first group and/or the second
- 15 group with a minimum of 25% of identity with the whole sequences of said polypeptides.

Preferred compositions comprise combinations with the polypeptide of the second group having SEQ ID N° 159.

20

Others preferred compositions comprise combinations wherein the polypeptides of the first group have a sequence selected in the group comprising SEQ ID N° 14, 15, 17, 21, 22, 23, 28, 29, 30, 32, 36, 38, 39, 41-44, 46, 49, 50, 52 to 55, 58, 60,

25 63, 133-138.

The above-mentioned polypeptides of the first group and the polynucleotides coding for said polypeptides are disclosed in WO 03/074553 in the name of Mutabilis SA.

30

The polypeptide of SEQ ID N° 159 and the polynucleotides having SEQ ID N°160 coding for said polypeptides are disclosed in WO 0121636 in the name of New-York University.

The invention also relates to combinations wherein said homologous isolated antigenic polypeptides of the first group have at least 25% identity to a polypeptide having a sequence SEQ ID N° as above defined, more particularly having SEQ ID N°14, 15, 17, 21, 22, 23, 28, 29, 30, 32, 36, 38, 39, 41-44, 46, 49, 50, 52 to 55, 58, 60, 63, 133-138, or at least 25% identity to a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide having a sequence corresponding to said SEQ ID N°s, as determined using BLASTP or BLASTX with the default parameters.

The invention also relates to combinations comprising homologous isolated antigenic peptides of second group having at least 25% identity to a polypeptide having SEQ ID N°159.

The invention also relates to the use in combination of isolated polynucleotides coding for a polypeptide of the first group and of isolated polynucleotides coding for polypeptides a polypeptide of the second group such as above defined according to the universal genetic code and taking into account the degeneracy of this code. The term "polynucleotide" encompasses any nucleotidic sequence such as DNA, including cDNA, RNA, including mRNA.

The polynucleotides coding for the polypeptides of the first group have preferably sequences corresponding to SEQ ID N° 67 to SEQ ID N° 132 or 146 to 158.

More preferably, said polynucleotides have sequences corresponding to SEQ ID N° 80, 81, 83, 87, 88, 89, 94, 95, 96, 98, 102, 104, 105, 107-110, 112, 115, 116, 118, 119, 126, 127, 130, 132, 135, 146-151.



The polynucleotides coding for the polypeptides of the second group have preferably sequence SEQ ID N° 160 of homologs to said polynucleotides. Said homologs may have at least 25% identity to a polynucleotide having said sequences, or at least 25% identity to a fragment comprising at least 15, at least 30, at least 60, at least 90, at least 120, at least 150, at least 180 or more than 180 consecutive nucleotide of a polynucleotide having one of said SEQ ID N°s, as determined using BLASTN with the default parameters, and are encompassed by the invention inasmuch as they are capable of coding for a polypeptide having the antigenic properties of those according to the invention.

The present application is also aimed towards any expression vector comprising at least one isolated polynucleotides coding for a polypeptide of said first group and at least one polynucleotide coding for a polypeptide of said second group according to the universal genetic code and taking into account the degeneracy of this code. The term "polynucleotide" encompasses any nucleotidic sequence such as DNA, including cDNA, RNA, including mRNA.

Preferred vectors comprise polynucleotides coding for the polypeptides of the first group having preferably sequences corresponding to SEQ ID N°77 to SEQ ID N°132 or 146 to 158.

More preferred vectors comprise, polynucleotides having sequences corresponding to SEQ ID N° 80, 81, 83, 87, 88, 89, 94, 95, 96, 98, 102, 104, 105, 107-110, 112, 115, 116, 118, 119, 126, 127, 130, 132, 135, 146-151.

More preferred vectors further comprise polynucleotides coding for the polypeptides of the second group having sequence SEQ ID N° 160.

Said vectors may also comprise homologs to said polynucleotides. Said homologs may have at least 25% identity to a polynucleotide having said sequences, or at least 25% identity to a fragment comprising at least 15, at least 30, at least 60, at least 90, at least 120, at least 150, at least 180 or more than 180 consecutive nucleotide of a polynucleotide having one of said SEQ ID N°s, as determined using BLASTN with the default parameters, and are encompassed by the invention inasmuch as they are capable of coding for a polypeptide having the antigenic properties of those according to the invention.

The invention also relates to any cell transformed by genetic engineering, characterized in that it comprises, by transfection, at least one of polynucleotides coding for a polypeptide of said first group and at least one a polynucleotide coding for a polypeptide of said second group and/or at least one vector according to the invention, and/or in that said transformation induces the production by this cell of said polypeptides.

The combinations of said antigenic polypeptides are capable of inducing an antibody response for prevention of infections due to ExPEC strains regardless of the pathogenesis and of the infection site (UTI, pyelonephritis, sepsis, bacteremia, neonatal meningitis).

The invention thus relates to vaccine compositions specific to *E. coli* extra-intestinal infections, comprising an effective amount of at least one antigenic polypeptide or fragment thereof of said first group and at least one antigenic polypeptide or fragment thereof of the second group, with a carrier, particularly at least one polypeptide of SEQ ID N°1

to SEQ ID N°66 and 133-145 and the homologous polypeptides, and at least one polypeptide of SEQ ID N° 159.

Such vaccine compositions are particularly useful for preventing urinary system infections, pyelonephritis, sepsis, bacteremia, neonatal meningitis.

The vaccine compositions of the invention are indicated for :

- 10       - Immunodepressed patients, ideally before the start of the immunosuppressive therapy: patients suffering from cancer, diabetes, leukaemia, transplant patients, patients receiving long-term steroids therapy.
- Patients before surgery where there is a high risk of *E. coli* infections (abdominal surgery).
- 15       - In all these cases, the *E. coli* vaccine of the invention could be administered in association with a *Staphylococcus aureus* vaccine or a group B *Streptococcus* vaccine,
- Patients with recurrent UTI, especially after one episode of pyelonephritis,
- 20       - The prevention of neonatal infections will require vaccination of the mother, implying vaccination long before pregnancy to avoid potential problem. Ideally such a vaccine should be associated with a Group B
- 25       *Streptococcus* polysaccharide vaccine in order to also prevent late onset neonatal infections. It should be pointed out that the induction of a level of antibodies against B2/D *E. coli* in pregnant women would also prevent UTI, which are always a risk in the context of
- 30       a pregnancy.

The formulation and the dose of said vaccine compositions can be developed and adjusted by those skilled in the art as a function of the indication targeted, of the method of

administration desired, and of the patient under consideration (age, weight).

5 These compositions comprise one or more physiologically inert vehicles, and in particular any excipient suitable for the formulation and/or for the method of administration desired.

10 For example the vaccine could be a suspension of the purified polypeptide in sterile water with aluminium based mineral salt as adjuvant and be administered subcutaneously with a first and boosting injection.

15 The combinations of antibodies respectively raised against at least one polypeptides of said first group and at least one polypeptide of said second group are also part of the invention.

20 They are capable of binding to said polypeptides in physiological-type conditions (*in vivo* or mimicking *in vivo*) when administered to a human or animal organism, and ELISA-type conditions when said binding product is intended to be used in assays and methods *in vitro*. Such combinations of antibodies advantageously inhibit the extra-intestinal growth of ExPEX strains in human or animal.

25 The invention thus relates to pharmaceutical compositions comprising an effective amount of a combination of antibodies such as above defined.

30 Such pharmaceutical compositions are particularly useful for immunotherapy applications for treatment and prevention of severe infections in at risk populations such as neonates or patients undergoing surgical procedures, or having urinary tract infections to prevent septicemia. For these applications

specific human monoclonal antibody (Mab) will be derived from said peptides or polypeptides.

Such pharmaceutical compositions comprising an effective  
5 amount of a combination of antibodies such as above defined  
are also useful for treating neonatal infections, in  
association with antibodies against *Staphylococcus aureus*  
and/or antibodies against group B *Streptococcus*.

10 The methods for manufacturing such antibodies using the  
polypeptides of the combinations according to the invention  
are available to those skilled in the art. They are  
conventional methods which comprise, in particular, the  
immunization of animals such as rabbits and the harvesting of  
15 the serum produced, followed optionally by the purification of  
the serum obtained. A technique suitable for the production of  
monoclonal antibodies is that of Köhler and Milstein  
(Nature 1975, 256:495-497).

20 Said antibodies do not recognize the cells of the human or  
animal to which it is intended.

The antibodies or fragments thereof are advantageously  
humanized when intended for a human administration.

25

Alternatively, humanized Mab could be derived from murine or  
rat Mab specific of the antigen. These fully humanized Mab are  
constructed using conventional molecular techniques to graft  
complementarity-determining regions from the parent murine or  
30 rat antibacterial antibody into human IgG1 kappa heavy and  
light-chain frameworks.

The present invention is also aimed towards the use, of said  
combinations of at least one polypeptide of the first group,

particularly having SEQ ID N°14, 15, 17, 21, 22, 23, 28, 29, 30, 32, 36, 38, 39, 41-44, 46, 49, 50, 52 to 55, 58, 60, 63, 133-138, and one polypeptide of the second group, particularly having SEQ ID N° 159, said antibodies raised against said polypeptides or polynucleotides coding for said polypeptides for the diagnosis of the presence or absence of undesirable extra-intestinal *E. coli*, and/or for the diagnosis of an extra-intestinal *E. coli* infection.

10 The detection of the presence or absence of such compounds can in particular be carried out by nucleotide hybridization, by PCR amplification or by detection of their polypeptide products. Detection of the presence of such compounds makes it possible to conclude that a B2/D *E. coli* strain is present.

15 The invention also relates to pharmaceutical compositions for alleviating and/or preventing and/or treating an undesirable growth of *E. coli* comprising an effective amount of at least one polypeptide of said each group particularly having SEQ ID N°1-66 to 133-145, for the first group, and SEQ ID N° 159 for the second group, in combination with a pharmaceutically acceptable carrier.

25 Preferred pharmaceutical compositions comprise at least one polypeptide having SEQ ID N°14, 15, 17, 21, 22, 23, 28, 29, 30, 32, 36, 38, 39, 41-44, 46, 49, 50, 52 to 55, 58, 60, 63, 133-138, and at least one polypeptide having SEQ ID N° 159.

30 The present application is also aimed towards any use of a said combination of polypeptides such as above defined for the manufacture of a composition, in particular of a pharmaceutical composition, intended to alleviate and/or to prevent and/or to treat an undesirable growth of *E. coli*, such as an *E. coli* infection, (for example systemic and non-

diarrhoeal infections), the presence of extra-intestinal *E. coli* or a sanitary contamination.

The present invention is illustrated by the examples, which  
5 follow and which are given in a non limiting capacity.

Another example of vaccination to demonstrate immunogenicity of polypeptides:

10 Preparation of antigenic peptidic combinations

A polypeptide having SEQ ID N° 28 is purified from an *E.coli* strain or from an host cell containing a recombine.

15 Polypeptides having SEQ ID N° 28 and SEQ ID N° 159, respectively, are purified and conjugated with a toxin.

A physiologically inert carrier is added to the preparation, which is sterilized and can be injected parenterally,  
20 subcutaneously or intramuscularly.

Said composition can also be sprayed onto *mucosa* with the aid of a spray.

25 Said combination of polypeptides may be added to a child hood vaccine.

Protecting effect of said combination in mice infected by *E. coli*

30

A total of 100 µg of said purified combination of polypeptides was administered to Balb C mice according to usual procedure of immunization.

A decrease of mortality in immunized animals was observed compared to non-immunized animals.





C L A I M S

- 1/ Compositions of polypeptides specific to pathogenic strains comprising at least one polypeptide of a first group, having a sequence selected in the group comprising the sequences of SEQ ID N°1 to N°66 or 133-145 and at least one  
5 peptide of a second group, having SEQ ID N° 159, or homologous sequences of polypeptides of the first group and/or the second group with a minimum of 25% of identity with the whole sequences of said polypeptides.
- 10 2/ The compositions according to claim 1, wherein the polypeptides of the second group have SEQ ID N°159.
- 3/ The compositions of claim 1 or 2, wherein the polypeptides of the first group have SEQ ID N° 14, 15, 17, 21, 22, 23, 28,  
15 29, 30, 32, 36, 38, 39, 41-44, 46, 49, 50, 52 to 55, 58, 60, 63 or 133-138
- 4/ The compositions according to anyone of claims 1 to 3, wherein said homologues isolated antigenic polypeptides of the  
20 first group have at least 25% identity to a polypeptide having a sequence such as above defined in claim 1, more particularly having SEQ ID N°14, 15, 17, 21, 22, 23, 28, 29, 30, 32, 36, 38, 39, 41-44, 46, 49, 50, 52 to 55, 58, 60, 63, 133-138, or at least 25% identity to a fragment comprising at least 5, at  
25 least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide having a sequence corresponding to said SEQ ID N°s, as determined using BLASTP or BLASTX with the default parameters.
- 30 5/ The compositions according to anyone of claims 1 to 4, wherein said homologous isolated antigenic polypeptides of the

second group have at least 25% identity to a polypeptide having SEQ ID N° 159.

- 6/ An expression vector comprising at least one isolated  
5 polynucleotides coding for a polypeptide of said first group and at least one a polypeptide of said second group according to the universal genetic code and taking into account the degeneracy of this code.
- 10 7/ An expression vector according to claim 6, wherein the polynucleotides coding for the polypeptides of the first group have sequences corresponding to SEQ ID N° 67 to SEQ ID N° 132 or 146 to 158.
- 15 8/ An expression vector according to claim 7, wherein said polynucleotides have sequences corresponding to SEQ ID N° 80, 81, 83, 87, 88, 89, 94, 95, 96, 98, 102, 104, 105, 107-110, 112, 115, 116, 118, 119, 126, 127, 130, 132, 135, 146-151.
- 20 9/ An expression vector according to anyone of claims 6 to 8, wherein the polynucleotide coding for the polypeptide of the second group has SEQ ID N° 160.
- 10/ An expression vector according to anyone of claims 6 to 9,  
25 comprising an homolog to said polynucleotides, said homologs having at least 25% identity to a fragment comprising at least 15, at least 30, at least 60, at least 90, at least 120, at least 150, at least 180 or more than 180 consecutive nucleotide of a polynucleotide having one of said SEQ ID N°s,  
30 as determined using BLASTN with the default parameters, and are encompassed by the invention inasmuch as they are capable of coding for a polypeptide having the antigenic properties of those according to the invention.

11/ A host cell comprising an expression vector according to anyone of claims 6 to 10.

12/ Vaccine compositions specific to *E. coli* extra-intestinal  
5 infections, comprising an effective amount of at least one antigenic polypeptide or fragment thereof of said first group and at least one antigenic polypeptide or fragment thereof of the second group, with a carrier, particularly at least one polypeptide of SEQ ID N°1 to SEQ ID N°66 and 133-145 and  
10 homologous polypeptides, and at least one polypeptide of SEQ ID N° 159 and homologous peptides.

13/ The vaccine compositions of claim 12 for preventing urinary system infections, pyelonephritis, sepsis, bacteremia,  
15 neonatal meningitidis.

14/ The vaccine composition of claim 12 or 13, adapted to specific indication in combination with components directed against other bacteria, such as *S. Aureus* or group *B*  
20 *Streptococcus*, or other bacteria implicated in systemic infections.

15/ Compositions of antibodies specific to polypeptidesic antigens of pathogenic strains particularly to extra-  
25 intestinal *E. Coli* strains, comprising combinations of antibodies directed against at least one polypeptide of said first group and antibodies directed against at least one polypeptide of the second group such as defined in anyone of claims 1 to 5.

30

16/ Compositions according to claim 15, wherein said ~~and~~ antibodies are monoclonal antibodies.

17/ Pharmaceutical compositions comprising a combination of antibodies according to claim 15 or 16.

5 18/ Pharmaceutical compositions according to claim 17 comprising an effective amount of a combination of antibodies according to claim 15 or 16, for treating neonatal infections, in association with antibodies against *Staphylococcus aureus* and/or antibodies against group B *Streptococcus*.

10 19/ The use of a pharmaceutical composition according to claim 17 or 18 for treatment or prevention of severe infection due to Expec in neonates and patients at risk for such infections.

15 20/ Pharmaceutical compositions for alleviating and/or preventing and/or treating an undesirable growth of *E. Coli* comprising an effective amount of at least a composition according to anyone of claims 1 to 5, in combination with a pharmaceutically acceptable carrier.

**ABSTRACT**

The invention relates to compositions of polypeptides specific to pathogenic strains comprising at least one polypeptide of a first group, having a sequence selected in the group comprising the sequences of SEQ ID N°1 to N°66 or 133-145 and at least one peptide of a second group, having SEQ ID N° 159, or homologous sequences of polypeptides of the first group and/or the second group with a minimum of 25% of identity with the whole sequences of said polypeptides.

Application for the preparation of vaccine compositions specific to *E. coli* extra-intestinal infections.



SEQUENCE LISTING <110> MUTABILIS <120>  
 Comprising of polypeptides specific to pathogenic strains and their use  
 as vaccines and in immunotherapy <130> 2013 <160> 160 <170>  
 PatentIn version 3.1 <210> 1 <211> 163 <212> PRT <213> Escherichia  
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Ser Ala Gln Asp Phe Tyr Asn Pro Ala Val Thr Leu Tyr Val Asp Gly  
 100 105 110

Val Pro Gln Leu Ser Thr Asn Thr Ile Gln Ala Leu Thr Asp Val Gln  
 115 120 125

Ser Val Glu Leu Leu Arg Gly Pro Gln Gly Thr Leu Tyr Gly Lys Ser  
 130 135 140

Ala Gln Gly Gly Ile Ile Asn Ile Val Thr Gln Gln Pro Asp Ser Thr  
 145 150 155 160

Pro Arg Gly Tyr Ile Glu Gly Gly Val Ser Ser Arg Asp Ser Tyr Arg  
 165 170 175

Ser Lys Phe Asn Leu Ser Gly Pro Ile Gln Asp Gly Leu Leu Tyr Gly  
 180 185 190

Ser Val Thr Leu Leu Arg Gln Val Asp Asp Gly Asp Met Ile Asn Pro  
 195 200 205

Ala Thr Gly Ser Asp Asp Leu Gly Gly Thr Arg Ala Ser Ile Gly Asn  
 210 215 220

Val Lys Leu Arg Leu Ala Pro Asp Asp Gln Pro Trp Glu Met Gly Phe  
 225 230 235 240

Ala Ala Ser Arg Glu Cys Thr Arg Ala Thr Gln Asp Ala Tyr Val Gly  
 245 250 255

Trp Asn Asp Ile Lys Gly Arg Lys Leu Ser Ile Ser Asp Gly Ser Pro  
 260 265 270

Asp Pro Tyr Met Arg Arg Cys Thr Asp Ser Gln Thr Leu Ser Gly Lys  
 275 280 285

Tyr Thr Thr Asp Asp Trp Val Phe Asn Leu Ile Ser Ala Trp Gln Gln  
 290 295 300

Gln His Tyr Ser Arg Thr Phe Pro Ser Gly Ser Leu Ile Val Asn Met  
 305 310 315 320

Ser Gln Arg Trp Asn Gln Asp Val Gln Glu Leu Arg Ala Ala Thr Leu  
 325 330 335

Gly Asp Ala Arg Thr Val Asp Met Val Phe Gly Leu Tyr Arg Gln Asn  
 340 345 350

Thr Arg Glu Lys Leu Asn Ser Ala Tyr Asp Met Pro Thr Met Pro Tyr  
 355 360 365

Leu Ser Ser Thr Gly Tyr Thr Thr Ala Glu Thr Leu Ala Ala Tyr Ser  
 370 375 380

Asp Leu Thr Trp His Leu Thr Asp Arg Phe Asp Ile Gly Gly Gly Val  
 385 390 395 400

Arg Phe Ser His Asp Lys Ser Ser Thr Gln Tyr His Gly Ser Met Leu  
 405 410 415

Gly Asn Pro Phe Gly Asp Gln Gly Lys Ser Asn Asp Asp Gln Val Leu  
 420 425 430

Gly Gln Leu Ser Ala Gly Tyr Met Leu Thr Asp Asp Trp Arg Val Tyr  
 435 440 445

Thr Arg Val Ala Gln Gly Tyr Lys Pro Ser Gly Tyr Asn Ile Val Pro  
 450 455 460

Thr Ala Gly Leu Asp Ala Lys Pro Phe Val Ala Glu Lys Ser Ile Asn  
 465 470 475 480

Tyr Glu Leu Gly Thr Arg Tyr Glu Thr Ala Asp Val Thr Leu Gln Ala  
 485 490 495

Ala Thr Phe Tyr Thr His Thr Lys Asp Met Gln Leu Tyr Ser Gly Pro  
 500 505 510

Val Gly Met Gln Thr Leu Ser Asn Ala Gly Lys Ala Asp Ala Thr Gly  
 515 520 525

Val Glu Leu Glu Ala Lys Trp Arg Phe Ala Pro Gly Trp Ser Trp Asp  
 530 535 540

Ile Asn Gly Asn Val Ile Arg Ser Glu Phe Thr Asn Asp Ser Glu Leu  
 545 550 555 560

Tyr His Gly Asn Arg Val Pro Phe Val Pro Arg Tyr Gly Ala Gly Ser  
 565 570 575

Ser Val Asn Gly Val Ile Asp Thr Arg Tyr Gly Ala Leu Met Pro Arg  
 580 585 590

Leu Ala Val Asn Leu Val Gly Pro His Tyr Phe Asp Gly Asp Asn Gln  
595 600 605

Leu Arg Gln Gly Thr Tyr Ala Thr Leu Asp Ser Ser Leu Gly Trp Gln  
610 615 620

Ala Thr Glu Arg Met Asn Ile Ser Val Tyr Val Asp Asn Leu Phe Asp  
625 630 635 640

Arg Arg Tyr Arg Thr Tyr Gly Tyr Met Asn Gly Ser Ser Ala Val Ala  
645 650 655

Gln Val Asn Met Gly Arg Thr Val Gly Ile Asn Thr Arg Ile Asp Phe  
660 665 670

Phe

<210> 3 <211> 246 <212> PRT <213> Escherichia coli <400> 3

Met Asn Lys Val Phe Val Val Ser Val Val Ala Ala Ala Cys Val Phe  
1 5 10 15

Ala Val Asn Ala Gly Ala Lys Glu Gly Lys Ser Gly Phe Tyr Leu Thr  
20 25 30

Gly Lys Ala Gly Ala Ser Val Met Ser Leu Ser Asp Gln Arg Phe Leu  
35 40 45

Ser Gly Asp Glu Glu Glu Thr Ser Lys Tyr Lys Gly Gly Asp Asp His  
50 55 60

Asp Thr Val Phe Ser Gly Gly Ile Ala Val Gly Tyr Asp Phe Tyr Pro  
65 70 75 80

Gln Phe Ser Ile Pro Val Arg Thr Glu Leu Glu Phe Tyr Ala Arg Gly  
85 90 95

Lys Ala Asp Ser Lys Tyr Asn Val Asp Lys Asp Ser Trp Ser Gly Gly  
100 105 110

Tyr Trp Arg Asp Asp Leu Lys Asn Glu Val Ser Val Asn Thr Leu Met  
115 120 125

Leu Asn Ala Tyr Tyr Asp Phe Arg Asn Asp Ser Ala Phe Thr Pro Trp  
130 135 140

Val Ser Ala Gly Ile Gly Tyr Ala Arg Ile His Gln Lys Thr Thr Gly  
145 150 155 160

Ile Ser Thr Trp Asp Tyr Glu Tyr Gly Ser Ser Gly Arg Glu Ser Leu  
 165 170 175  
 Ser Arg Ser Gly Ser Ala Asp Asn Phe Ala Trp Ser Leu Gly Ala Gly  
 180 185 190  
 Val Arg Tyr Asp Val Thr Pro Asp Ile Ala Leu Asp Leu Ser Tyr Arg  
 195 200 205  
 Tyr Leu Asp Ala Gly Asp Ser Ser Val Ser Tyr Lys Asp Glu Trp Gly  
 210 215 220  
 Asp Lys Tyr Lys Ser Glu Val Asp Val Lys Ser His Asp Ile Met Leu  
 225 230 235 240  
 Gly Met Thr Tyr Asn Phe  
 245  
 <210> 4 <211> 166 <212> PRT <213> Escherichia coli <400> 4  
 Met Lys Leu Lys Ala Ile Ile Leu Ala Thr Gly Leu Ile Asn Cys Ile  
 1 5 10 15  
 Ala Phe Ser Ala Gln Ala Val Asp Thr Thr Ile Thr Val Thr Gly Arg  
 20 25 30  
 Val Leu Pro Arg Thr Cys Thr Ile Gly Asn Gly Gly Asn Pro Asn Ala  
 35 40 45  
 Thr Val Val Leu Asp Asn Ala Tyr Thr Ser Asp Leu Ile Ala Ala Asn  
 50 55 60  
 Ser Thr Ser Gln Trp Lys Asn Phe Ser Leu Thr Leu Thr Asn Cys Gln  
 65 70 75 80  
 Asn Val Asn Asn Val Thr Ser Phe Gly Gly Thr Ala Glu Asn Thr Asn  
 85 90 95  
 Tyr Tyr Arg Asn Thr Gly Asp Ala Thr Asn Ile Met Val Glu Leu Gln  
 100 105 110  
 Glu Gln Gly Asn Gly Asn Thr Pro Leu Lys Val Gly Ser Thr Lys Val  
 115 120 125  
 Val Thr Val Ser Asn Gly Gln Ala Thr Phe Asn Leu Lys Val Arg Ala  
 130 135 140  
 Val Ser Lys Gly Asn Ala Gly Ala Gly Ser Ile Asn Ser Gln Ile Thr  
 145 150 155 160

Val Thr Tyr Thr Tyr Ala  
165

<210> 5 <211> 1295 <212> PRT <213> Escherichia coli <400> 5

Met Asn Lys Ile Tyr Ser Leu Lys Tyr Ser Ala Ala Thr Gly Gly Leu  
1 5 10 15

Ile Ala Val Ser Glu Leu Ala Lys Arg Val Ser Gly Lys Thr Asn Arg  
20 25 30

Lys Leu Val Ala Thr Met Leu Ser Leu Ala Val Ala Gly Thr Val Asn  
35 40 45

Ala Ala Asn Ile Asp Ile Ser Asn Val Trp Ala Arg Asp Tyr Leu Asp  
50 55 60

Leu Ala Gln Asn Lys Gly Ile Phe Gln Pro Gly Ala Thr Asp Val Thr  
65 70 75 80

Ile Thr Leu Lys Asn Gly Asp Lys Phe Ser Phe His Asn Leu Ser Ile  
85 90 95

Pro Asp Phe Ser Gly Ala Ala Ala Ser Gly Ala Ala Thr Ala Ile Gly  
100 105 110

Gly Ser Tyr Ser Val Thr Val Ala His Asn Lys Lys Asn Pro Gln Ala  
115 120 125

Ala Glu Thr Gln Val Tyr Ala Gln Ser Ser Tyr Arg Val Val Asp Arg  
130 135 140

Arg Asn Ser Asn Asp Phe Glu Ile Gln Arg Leu Asn Lys Phe Val Val  
145 150 155 160

Glu Thr Val Gly Ala Thr Pro Ala Glu Thr Asn Pro Thr Thr Tyr Ser  
165 170 175

Asp Ala Leu Glu Arg Tyr Gly Ile Val Thr Ser Asp Gly Ser Lys Lys  
180 185 190

Ile Ile Gly Phe Arg Ala Gly Ser Gly Gly Thr Ser Phe Ile Asn Gly  
195 200 205

Glu Ser Lys Ile Ser Thr Asn Ser Ala Tyr Ser His Asp Leu Leu Ser  
210 215 220

Ala Ser Leu Phe Glu Val Thr Gln Trp Asp Ser Tyr Gly Met Met Ile  
225 230 235 240

Tyr Lys Asn Asp Lys Thr Phe Arg Asn Leu Glu Ile Phe Gly Asp Ser  
 245 250 255  
 Gly Ser Gly Ala Tyr Leu Tyr Asp Asn Lys Leu Glu Lys Trp Val Leu  
 260 265 270  
 Val Gly Thr Thr His Gly Ile Ala Ser Val Asn Gly Asp Gln Leu Thr  
 275 280 285  
 Trp Ile Thr Lys Tyr Asn Asp Lys Leu Val Ser Glu Leu Lys Asp Thr  
 290 295 300  
 Tyr Ser His Lys Ile Asn Leu Asn Gly Asn Asn Val Thr Ile Lys Asn  
 305 310 315 320  
 Thr Asp Ile Thr Leu His Gln Asn Asn Ala Asp Thr Thr Gly Thr Gln  
 325 330 335  
 Glu Lys Ile Thr Lys Asp Lys Asp Ile Val Phe Thr Asn Gly Gly Asp  
 340 345 350  
 Val Leu Phe Lys Asp Asn Leu Asp Phe Gly Ser Gly Gly Ile Ile Phe  
 355 360 365  
 Asp Glu Gly His Glu Tyr Asn Ile Asn Gly Gln Gly Phe Thr Phe Lys  
 370 375 380  
 Gly Ala Gly Ile Asp Ile Gly Lys Glu Ser Ile Val Asn Trp Asn Ala  
 385 390 395 400  
 Leu Tyr Ser Ser Asp Asp Val Leu His Lys Ile Gly Pro Gly Thr Leu  
 405 410 415  
 Asn Val Gln Lys Lys Gln Gly Ala Asn Ile Lys Ile Gly Glu Gly Asn  
 420 425 430  
 Val Ile Leu Asn Glu Glu Gly Thr Phe Asn Asn Ile Tyr Leu Ala Ser  
 435 440 445  
 Gly Asn Gly Lys Val Ile Leu Asn Lys Asp Asn Ser Leu Gly Asn Asp  
 450 455 460  
 Gln Tyr Ala Gly Ile Phe Phe Thr Lys Arg Gly Gly Thr Leu Asp Leu  
 465 470 475 480  
 Asn Gly His Asn Gln Thr Phe Thr Arg Ile Ala Ala Thr Asp Asp Gly  
 485 490 495

Thr Thr Ile Thr Asn Ser Asp Thr Thr Lys Glu Ala Val Leu Ala Ile  
500 505 510

Asn Asn Glu Asp Ser Tyr Ile Tyr His Gly Asn Ile Asn Gly Asn Ile  
515 520 525

Lys Leu Thr His Asn Ile Asn Ser Gln Asp Lys Lys Thr Asn Ala Lys  
530 535 540

Leu Ile Leu Asp Gly Ser Val Asn Thr Lys Asn Asp Val Glu Val Ser  
545 550 555 560

Asn Ala Ser Leu Thr Met Gln Gly His Ala Thr Glu His Ala Ile Phe  
565 570 575

Arg Ser Ser Ala Asn His Cys Ser Leu Val Phe Leu Cys Gly Thr Asp  
580 585 590

Trp Val Thr Val Leu Lys Glu Thr Glu Ser Ser Tyr Asn Lys Lys Phe  
595 600 605

Asn Ser Asp Tyr Lys Ser Asn Asn Gln Gln Thr Ser Phe Asp Gln Pro  
610 615 620

Asp Trp Lys Thr Gly Val Phe Lys Phe Asp Thr Leu His Leu Asn Asn  
625 630 635 640

Ala Asp Phe Ser Ile Ser Arg Asn Ala Asn Val Glu Gly Asn Ile Ser  
645 650 655

Ala Asn Lys Ser Ala Ile Thr Ile Gly Asp Lys Asn Val Tyr Ile Asp  
660 665 670

Asn Leu Ala Gly Lys Asn Ile Thr Asn Asn Gly Phe Asp Phe Lys Gln  
675 680 685

Thr Ile Ser Thr Asn Leu Ser Ile Gly Glu Thr Lys Phe Thr Gly Gly  
690 695 700

Ile Thr Ala His Asn Ser Gln Ile Ala Ile Gly Asp Gln Ala Val Val  
705 710 715 720

Thr Leu Asn Gly Ala Thr Phe Leu Asp Asn Thr Pro Ile Ser Ile Asp  
725 730 735

Lys Gly Ala Lys Val Ile Ala Gln Asn Ser Met Phe Thr Thr Lys Gly  
740 745 750

Ile Asp Ile Ser Gly Glu Leu Thr Met Met Gly Ile Pro Glu Gln Asn  
755 760 765

Ser Lys Thr Val Thr Pro Gly Leu His Tyr Ala Ala Asp Gly Phe Arg  
 770 775 780

Leu Ser Gly Gly Asn Ala Asn Phe Ile Ala Arg Asn Met Ala Ser Val  
 785 790 795 800

Thr Gly Asn Ile Tyr Ala Asp Asp Ala Ala Thr Ile Thr Leu Gly Gln  
 805 810 815

Pro Glu Thr Glu Thr Pro Thr Ile Ser Ser Ala Tyr Gln Ala Trp Ala  
 820 825 830

Glu Thr Leu Leu Tyr Gly Phe Asp Thr Ala Tyr Arg Gly Ala Ile Thr  
 835 840 845

Ala Pro Lys Ala Thr Val Ser Met Asn Asn Ala Ile Trp His Leu Asn  
 850 855 860

Ser Gln Ser Ser Ile Asn Arg Leu Glu Thr Lys Asp Ser Met Val Arg  
 865 870 875 880

Phe Thr Gly Asp Asn Gly Lys Phe Thr Thr Leu Thr Val Asn Asn Leu  
 885 890 895

Thr Ile Asp Asp Ser Ala Phe Val Leu Arg Ala Asn Leu Ala Gln Ala  
 900 905 910

Asp Gln Leu Val Val Asn Lys Ser Leu Ser Gly Lys Asn Asn Leu Leu  
 915 920 925

Leu Val Asp Phe Ile Glu Lys Asn Gly Asn Ser Asn Gly Leu Asn Ile  
 930 935 940

Asp Leu Val Ser Ala Pro Lys Gly Thr Ala Val Asp Val Phe Lys Ala  
 945 950 955 960

Thr Thr Arg Ser Ile Gly Phe Ser Asp Val Thr Pro Val Ile Glu Gln  
 965 970 975

Lys Asn Asp Thr Asp Lys Ala Thr Trp Thr Leu Ile Gly Tyr Lys Ser  
 980 985 990

Val Ala Ash Ala Asp Ala Ala Lys Lys Ala Thr Leu Leu Met Ser Gly  
 995 1000 1005

Gly Tyr Lys Ala Phe Leu Ala Glu Val Asn Asn Leu Asn Lys Arg  
 1010 1015 1020



Met Gly Asp Leu Arg Asp Ile Asn Gly Glu Ser Gly Ala Trp Ala  
1025 1030 1035

Arg Ile Ile Ser Gly Thr Gly Ser Ala Gly Gly Gly Phe Ser Asp  
1040 1045 1050

Asn Tyr Thr His Val Gln Val Gly Ala Asp Asn Lys His Glu Leu  
1055 1060 1065

Asp Gly Leu Asp Leu Phe Thr Gly Val Thr Met Thr Tyr Thr Asp  
1070 1075 1080

Ser His Ala Gly Ser Asp Ala Phe Ser Gly Glu Thr Lys Ser Val  
1085 1090 1095

Gly Ala Gly Leu Tyr Ala Ser Ala Met Phe Glu Ser Gly Ala Tyr  
1100 1105 1110

Ile Asp Leu Ile Gly Lys Tyr Val His His Asp Asn Glu Tyr Thr  
1115 1120 1125

Ala Thr Phe Ala Gly Leu Gly Thr Arg Asp Tyr Ser Ser His Ser  
1130 1135 1140

Trp Tyr Ala Gly Ala Glu Val Gly Tyr Arg Tyr His Val Thr Asp  
1145 1150 1155

Ser Ala Trp Ile Glu Pro Gln Ala Glu Leu Val Tyr Gly Ala Val  
1160 1165 1170

Ser Gly Lys Gln Phe Ser Trp Lys Asp Gln Gly Met Asn Leu Thr  
1175 1180 1185

Met Lys Asp Lys Asp Phe Asn Pro Leu Ile Gly Arg Thr Gly Val  
1190 1195 1200

Asp Val Gly Lys Ser Phe Ser Gly Lys Asp Trp Lys Val Thr Ala  
1205 1210 1215

Arg Ala Gly Leu Gly Tyr Gln Phe Asp Leu Phe Ala Asn Gly Glu  
1220 1225 1230

Thr Val Leu Arg Asp Ala Ser Gly Glu Lys Arg Ile Lys Gly Glu  
1235 1240 1245

Lys Asp Gly Arg Met Leu Met Asn Val Gly Leu Asn Ala Glu Ile  
1250 1255 1260

Arg Asp Asn Leu Arg Phe Gly Leu Glu Phe Glu Lys Ser Ala Phe  
1265 1270 1275

Gly Lys Tyr Asn Val Asp Asn Ala Ile Asn Ala Asn Phe Arg Tyr  
 1280 1285 1290

Ser Phe  
 1295

<210> 6 <211> 142 <212> PRT <213> Escherichia coli <400> 6

Met Ile Asn Ile Pro Ser Pro Thr Ala Val Val Met Ala Leu Val Ala  
 1 5 10 15

Ile Ser Thr Leu Pro Ser Pro Ser Arg Val Lys Leu Met Pro Tyr Pro  
 20 25 30

Pro Arg Ala His Asn Thr Thr Gly Leu Leu Pro Val Arg Glu Ile Cys  
 35 40 45

Phe Pro His His Gly Asp Asp Gly Arg Asn Ser Ile Glu Pro Ser Ile  
 50 55 60

Ser Arg Ala Ala His Thr Asp Arg Leu Arg Phe Val Cys Met Thr Arg  
 65 70 75 80

Thr Gly Ser Thr Thr Ser Arg Pro Phe Cys Pro Ile Pro Arg Ser Pro  
 85 90 95

Ala Leu Asn Ala Ser Gly Gln Gln Asp Ser Gly Phe Trp Gly Val Ser  
 100 105 110

Ser Ile Pro Gly Asp Ile Leu Met Phe Gln Leu His Val Leu Ile Val  
 115 120 125

Phe Ile Cys Lys Ile Asn Leu Ser Asp Asn Asn Ile Ser Tyr  
 130 135 140

<210> 7 <211> 318 <212> PRT <213> Escherichia coli <400> 7

Met Tyr Ala Arg Glu Tyr Arg Ser Thr Arg Pro His Lys Ala Ile Phe  
 1 5 10 15

Phe His Leu Ser Cys Leu Thr Leu Ile Cys Ser Ala Gln Val Tyr Ala  
 20 25 30

Lys Pro Asp Met Arg Pro Leu Gly Pro Asn Ile Ala Asp Lys Gly Ser  
 35 40 45

Val Phe Tyr His Phe Ser Ala Thr Ser Phe Asp Ser Val Asp Gly Thr  
 50 55 60

Arg His Tyr Arg Val Trp Thr Ala Val Pro Asn Thr Thr Ala Pro Ala  
65 70 75 80

Ser Gly Tyr Pro Ile Leu Tyr Met Leu Asp Gly Asn Ala Val Met Asp  
85 90 95

Arg Leu Asp Asp Glu Leu Leu Lys Gln Leu Ser Glu Lys Thr Pro Pro  
100 105 110

Val Ile Val Ala Val Gly Tyr Gln Thr Asn Leu Pro Phe Asp Leu Asn  
115 120 125

Ser Arg Ala Tyr Asp Tyr Thr Pro Ala Ala Glu Ser Arg Lys Thr Asp  
130 135 140

Leu His Ser Gly Arg Phe Ser Arg Lys Ser Gly Gly Ser Asn Asn Phe  
145 150 155 160

Arg Gln Leu Leu Glu Thr Arg Ile Ala Pro Lys Val Glu Gln Gly Leu  
165 170 175

Asn Ile Asp Arg Gln Arg Arg Gly Leu Trp Gly His Ser Tyr Gly Gly  
180 185 190

Leu Phe Val Leu Asp Ser Trp Leu Ser Ser Ser Tyr Phe Arg Ser Tyr  
195 200 205

Tyr Ser Ala Ser Pro Ser Leu Gly Arg Gly Tyr Asp Ala Leu Leu Ser  
210 215 220

Arg Val Thr Ala Val Glu Pro Leu Gln Phe Cys Thr Lys His Leu Ala  
225 230 235 240

Ile Met Glu Gly Ser Ala Thr Gln Gly Asp Asn Arg Glu Thr His Ala  
245 250 255

Val Gly Val Leu Ser Lys Ile His Thr Thr Leu Thr Ile Leu Lys Asp  
260 265 270

Lys Gly Val Asn Ala Val Phe Trp Asp Phe Pro Asn Leu Gly His Gly  
275 280 285

Pro Met Phe Asn Ala Ser Phe Arg Gln Ala Leu Leu Asp Ile Ser Gly  
290 295 300

Glu Asn Ala Asn Tyr Thr Ala Gly Cys His Glu Leu Ser His  
305 310 315

<210> 8 <211> 725 <212> PRT <213> Escherichia coli <400> 8

Met Arg Ile Asn Lys Ile Leu Trp Ser Leu Thr Val Leu Leu Val Gly  
 1 5 10 15  
 Leu Asn Ser Gln Val Ser Val Ala Lys Tyr Ser Asp Asp Asp Asn Asp  
 20 25 30  
 Glu Thr Leu Val Val Glu Ala Thr Ala Glu Gln Val Leu Lys Gln Gln  
 35 40 45  
 Pro Gly Val Ser Val Ile Thr Ser Glu Asp Ile Lys Lys Thr Pro Pro  
 50 55 60  
 Val Asn Asp Leu Ser Asp Ile Ile Arg Lys Met Pro Gly Val Asn Leu  
 65 70 75 80  
 Thr Gly Asn Ser Ala Ser Gly Thr Arg Gly Asn Asn Arg Gln Ile Asp  
 85 90 95  
 Ile Arg Gly Met Gly Pro Glu Asn Thr Leu Ile Leu Ile Asp Gly Val  
 100 105 110  
 Pro Val Thr Ser Arg Asn Ser Val Arg Tyr Ser Trp Arg Gly Glu Arg  
 115 120 125  
 Asp Thr Arg Gly Asp Thr Asn Trp Val Pro Pro Glu Gln Val Glu Arg  
 130 135 140  
 Ile Glu Val Ile Arg Gly Pro Ala Ala Ala Arg Tyr Gly Ser Gly Ala  
 145 150 155 160  
 Ala Gly Gly Val Val Asn Ile Ile Thr Lys Arg Pro Thr Asn Asp Trp  
 165 170 175  
 His Gly Ser Leu Ser Leu Tyr Thr Asn Gln Pro Glu Ser Ser Glu Glu  
 180 185 190  
 Gly Ala Thr Arg Arg Ala Asn Phe Ser Leu Ser Gly Pro Leu Ala Gly  
 195 200 205  
 Asp Ala Leu Thr Thr Arg Leu Tyr Gly Asn Leu Asn Lys Thr Asp Ala  
 210 215 220  
 Asp Ser Trp Asp Ile Asn Ser Pro Val Gly Thr Lys Asn Ala Ala Gly  
 225 230 235 240  
 His Glu Gly Val Arg Asn Lys Asp Ile Asn Gly Val Val Ser Trp Lys  
 245 250 255  
 Leu Asn Pro Gln Gln Ile Leu Asp Phe Glu Val Gly Tyr Ser Arg Gln  
 260 265 270

Gly Asn Ile Tyr Ala Gly Asp Thr Gln Asn Ser Ser Ser Ser Ala Val  
 275 280 285

Thr Glu Ser Leu Ala Lys Ser Gly Lys Glu Thr Asn Arg Leu Tyr Arg  
 290 295 300

Gln Asn Tyr Gly Ile Thr His Asn Gly Ile Trp Asp Trp Gly Gln Ser  
 305 310 315 320

Arg Phe Gly Val Tyr Tyr Glu Lys Thr Asn Asn Thr Arg Met Asn Glu  
 325 330 335

Gly Leu Ser Gly Gly Gly Glu Gly Arg Ile Leu Ala Gly Glu Lys Phe  
 340 345 350

Thr Thr Asn Arg Leu Ser Ser Trp Arg Thr Ser Gly Glu Leu Asn Ile  
 355 360 365

Pro Leu Asn Val Met Val Asp Gln Thr Leu Thr Val Gly Ala Glu Trp  
 370 375 380

Asn Arg Asp Lys Leu Asp Asp Pro Ser Ser Thr Ser Leu Thr Val Asn  
 385 390 395 400

Asp Arg Asp Ile Ser Gly Ile Ser Gly Ser Ala Ala Asp Arg Ser Ser  
 405 410 415

Lys Asn His Ser Gln Ile Ser Ala Leu Tyr Ile Glu Asp Asn Ile Glu  
 420 425 430

Pro Val Pro Gly Thr Asn Ile Ile Pro Gly Leu Arg Phe Asp Tyr Leu  
 435 440 445

Ser Asp Ser Gly Gly Asn Phe Ser Pro Ser Leu Asn Leu Ser Gln Glu  
 450 455 460

Leu Gly Asp Tyr Phe Lys Val Lys Ala Gly Val Ala Arg Thr Phe Lys  
 465 470 475 480

Ala Pro Asn Leu Tyr Gln Ser Ser Glu Gly Tyr Leu Leu Tyr Ser Lys  
 485 490 495

Gly Asn Gly Cys Pro Lys Asp Ile Thr Ser Gly Gly Cys Tyr Leu Ile  
 500 505 510

Gly Asn Lys Asp Leu Asp Pro Glu Ile Ser Val Asn Lys Glu Ile Gly  
 515 520 525

Leu Glu Phe Thr Trp Glu Asp Tyr His Ala Ser Val Thr Tyr Phe Arg  
530 535 540

Asn Asp Tyr Gln Asn Lys Ile Val Ala Gly Asp Asn Val Ile Gly Gln  
545 550 555 560

Thr Ala Ser Gly Ala Tyr Ile Leu Lys Trp Gln Asn Gly Gly Lys Ala  
565 570 575

Leu Val Asp Gly Ile Glu Ala Ser Met Ser Phe Pro Leu Val Lys Glu  
580 585 590

Arg Leu Asn Trp Asn Thr Asn Ala Thr Trp Met Ile Thr Ser Glu Gln  
595 600 605

Lys Asp Thr Gly Asn Pro Leu Ser Val Ile Pro Lys Tyr Thr Ile Asn  
610 615 620

Asn Ser Leu Asn Trp Thr Ile Thr Gln Ala Phe Ser Ala Ser Phe Asn  
625 630 635 640

Trp Thr Leu Tyr Gly Arg Gln Lys Pro Arg Thr His Ala Glu Thr Arg  
645 650 655

Ser Glu Asp Thr Gly Gly Leu Ser Gly Lys Glu Leu Gly Ala Tyr Ser  
660 665 670

Leu Val Gly Thr Asn Phe Asn Tyr Asp Ile Asn Lys Asn Leu Arg Leu  
675 680 685

Asn Val Gly Val Ser Asn Ile Leu Asn Lys Gln Ile Phe Arg Ser Ser  
690 695 700

Glu Gly Ala Asn Thr Tyr Asn Glu Pro Gly Arg Ala Tyr Tyr Ala Gly  
705 710 715 720

Val Thr Ala Ser Phe  
725

<210> 9 <211> 1014 <212> PRT <213> Escherichia coli <400> 9

Met Gly Asn Gln Trp Gln Gln Lys Tyr Leu Leu Glu Tyr Asn Glu Leu  
1 5 10 15

Val Ser Asn Phe Pro Ser Pro Glu Arg Val Val Ser Asp Tyr Ile Lys  
20 25 30

Asn Cys Phe Lys Thr Asp Leu Pro Trp Phe Ser Arg Ile Asp Pro Asp  
35 40 45

Asn Ala Tyr Phe Ile Cys Phe Ser Gln Asn Arg Ser Asn Ser Arg Ser  
 50 55 60  
 Tyr Thr Gly Trp Asp His Leu Gly Lys Tyr Lys Thr Glu Val Leu Thr  
 65 70 75 80  
 Leu Thr Gln Ala Ala Leu Ile Asn Ile Gly Tyr Arg Phe Asp Val Phe  
 85 90 95  
 Asp Asp Ala Asn Ser Ser Thr Gly Ile Tyr Lys Thr Lys Ser Ala Asp  
 100 105 110  
 Val Phe Asn Glu Glu Asn Glu Glu Lys Met Leu Pro Ser Glu Tyr Leu  
 115 120 125  
 His Phe Leu Gln Lys Cys Asp Phe Ala Gly Val Tyr Gly Lys Thr Leu  
 130 135 140  
 Ser Asp Tyr Trp Ser Lys Tyr Tyr Asp Lys Phe Lys Leu Leu Leu Lys  
 145 150 155 160  
 Asn Tyr Tyr Ile Ser Ser Ala Leu Tyr Leu Tyr Lys Asn Gly Glu Leu  
 165 170 175  
 Asp Glu Arg Glu Tyr Asn Phe Ser Met Asn Ala Leu Asn Arg Ser Asp  
 180 185 190  
 Asn Ile Ser Leu Leu Phe Phe Asp Ile Tyr Gly Tyr Tyr Ala Ser Asp  
 195 200 205  
 Ile Phe Val Ala Lys Asn Asn Asp Lys Val Met Leu Phe Ile Pro Gly  
 210 215 220  
 Ala Lys Lys Pro Phe Leu Phe Lys Lys Asn Ile Ala Asp Leu Arg Leu  
 225 230 235 240  
 Thr Leu Lys Glu Leu Ile Lys Asp Ser Asp Asn Lys Gln Leu Leu Ser  
 245 250 255  
 Gln His Phe Ser Leu Tyr Ser Arg Gln Asp Gly Val Ser Tyr Ala Gly  
 260 265 270  
 Val Asn Ser Val Leu His Ala Ile Glu Asn Asp Gly Asn Phe Asn Glu  
 275 280 285  
 Ser Tyr Phe Leu Tyr Ser Asn Lys Thr Leu Ser Asn Lys Asp Val Phe  
 290 295 300  
 Asp Ala Ile Ala Ile Ser Val Lys Lys Arg Ser Phe Ser Asp Gly Asp  
 305 310 315 320

Ile Val Ile Lys Ser Asn Ser Glu Ala Gln Arg Asp Tyr Ala Leu Thr  
 325 330 335  
 Ile Leu Gln Thr Ile Leu Ser Met Thr Pro Ile Phe Asp Ile Val Val  
 340 345 350  
 Pro Glu Val Ser Val Pro Leu Gly Leu Gly Ile Ile Thr Ser Ser Met  
 355 360 365  
 Gly Ile Ser Phe Asp Gln Leu Ile Asn Gly Asp Thr Tyr Glu Glu Arg  
 370 375 380  
 Arg Ser Ala Ile Pro Gly Leu Ala Thr Asn Ala Val Leu Leu Gly Leu  
 385 390 395 400  
 Ser Phe Ala Ile Pro Leu Leu Ile Ser Lys Ala Gly Ile Asn Gln Glu  
 405 410 415  
 Val Leu Ser Ser Val Ile Asn Asn Glu Gly Arg Thr Leu Asn Glu Thr  
 420 425 430  
 Asn Ile Asp Ile Phe Leu Lys Glu Tyr Gly Ile Ala Glu Asp Ser Ile  
 435 440 445  
 Ser Ser Thr Asn Leu Leu Asp Val Lys Leu Lys Ser Ser Gly Gln His  
 450 455 460  
 Val Asn Ile Val Lys Leu Ser Asp Glu Asp Asn Gln Ile Val Ala Val  
 465 470 475 480  
 Lys Gly Ser Ser Leu Ser Gly Ile Tyr Tyr Glu Val Asp Ile Glu Thr  
 485 490 495  
 Gly Tyr Glu Ile Leu Ser Arg Arg Ile Tyr Arg Thr Glu Tyr Asn Asn  
 500 505 510  
 Glu Ile Leu Trp Thr Arg Gly Gly Gly Leu Lys Gly Gly Gln Pro Phe  
 515 520 525  
 Asp Phe Glu Ser Leu Asn Ile Pro Val Phe Phe Lys Asp Glu Pro Tyr  
 530 535 540  
 Ser Ala Val Thr Gly Ser Pro Leu Ser Phe Ile Asn Asp Asp Ser Ser  
 545 550 555 560  
 Leu Leu Tyr Pro Asp Thr Asn Pro Lys Leu Pro Gln Pro Thr Ser Glu  
 565 570 575



Met Asp Ile Val Asn Tyr Val Lys Gly Ser Gly Ser Phe Gly Asp Arg  
580 585 590

Phe Val Thr Leu Met Arg Gly Ala Thr Glu Glu Glu Ala Trp Asn Ile  
595 600 605

Ala Ser Tyr His Thr Ala Gly Gly Ser Thr Glu Glu Leu His Glu Ile  
610 615 620

Leu Leu Gly Gln Gly Pro Gln Ser Ser Leu Gly Phe Thr Glu Tyr Thr  
625 630 635 640

Ser Asn Val Asn Ser Ala Asp Ala Ala Ser Arg Arg His Phe Leu Val  
645 650 655

Val Ile Lys Val His Val Lys Tyr Ile Thr Asn Asn Asn Val Ser Tyr  
660 665 670

Val Asn His Trp Ala Ile Pro Asp Glu Ala Pro Val Glu Val Leu Ala  
675 680 685

Val Val Asp Arg Arg Phe Asn Phe Pro Glu Pro Ser Thr Pro Pro Asp  
690 695 700

Ile Ser Thr Ile Arg Lys Leu Leu Ser Leu Arg Tyr Phe Lys Glu Ser  
705 710 715 720

Ile Glu Ser Thr Ser Lys Ser Asn Phe Gln Lys Leu Ser Arg Gly Asn  
725 730 735

Ile Asp Val Leu Lys Gly Arg Gly Ser Ile Ser Ser Thr Arg Gln Arg  
740 745 750

Ala Ile Tyr Pro Tyr Phe Glu Ala Ala Asn Ala Asp Glu Gln Gln Pro  
755 760 765

Leu Phe Phe Tyr Ile Lys Lys Asp Arg Phe Asp Asn His Gly Tyr Asp  
770 775 780

Gln Tyr Phe Tyr Asp Asn Thr Val Gly Leu Asn Gly Ile Pro Thr Leu  
785 790 795 800

Asn Thr Tyr Thr Gly Glu Ile Pro Ser Asp Ser Ser Ser Leu Gly Ser  
805 810 815

Thr Tyr Trp Lys Lys Tyr Asn Leu Thr Asn Glu Thr Ser Ile Ile Arg  
820 825 830

Val Ser Asn Ser Ala Arg Gly Ala Asn Gly Ile Lys Ile Ala Leu Glu  
835 840 845

Glu Val Gln Glu Gly Lys Pro Val Ile Ile Thr Ser Gly Asn Leu Ser  
850 855 860

Gly Cys Thr Thr Ile Val Ala Arg Lys Glu Gly Tyr Ile Tyr Lys Val  
865 870 875 880

His Thr Gly Thr Thr Lys Ser Leu Ala Gly Phe Thr Ser Thr Thr Gly  
885 890 895

Val Lys Lys Ala Val Glu Val Leu Glu Leu Leu Thr Lys Glu Pro Ile  
900 905 910

Pro Arg Val Glu Gly Ile Met Ser Asn Asp Phe Leu Val Asp Tyr Leu  
915 920 925

Ser Glu Asn Phe Glu Asp Ser Leu Ile Thr Tyr Ser Ser Ser Glu Lys  
930 935 940

Lys Pro Asp Ser Gln Ile Thr Ile Ile Arg Asp Asn Val Ser Val Phe  
945 950 955 960

Pro Tyr Phe Leu Asp Asn Ile Pro Glu His Gly Phe Gly Thr Ser Ala  
965 970 975

Thr Val Leu Val Arg Val Asp Gly Asn Val Val Val Arg Ser Leu Ser  
980 985 990

Glu Ser Tyr Ser Leu Asn Ala Asp Ala Ser Glu Ile Ser Val Leu Lys  
995 1000 1005

Val Phe Ser Lys Lys Phe  
1010

<210> 10 <211> 454 <212> PRT <213> Escherichia coli <400> 10

Met Val Asp Met Ile Asn Glu Ser Ala Arg Gln Thr Pro Val Ile Ala  
1 5 10 15

Gln Thr Asp Val Leu Val Ile Gly Gly Gly Pro Ala Gly Leu Ser Ala  
20 25 30

Ala Ile Ala Ala Gly Arg Leu Gly Ala Arg Thr Met Ile Val Glu Arg  
35 40 45

Tyr Gly Ser Leu Gly Gly Val Leu Thr Gln Val Gly Val Glu Ser Phe  
50 55 60

Ala Trp Tyr Arg His Pro Gly Thr Glu Asp Cys Glu Gly Ile Cys Arg  
65 70 75 80

Glu Tyr Glu Gly Arg Ala Arg Ala Leu Gly Phe Thr Arg Pro Glu Pro  
 85 90 95  
 Gln Ser Ile Ser Glu Val Ile Asp Thr Glu Gly Phe Lys Val Val Ala  
 100 105 110  
 Asp Gln Met Ile Thr Glu Ser Gly Val Glu Pro Leu Tyr His Ser Trp  
 115 120 125  
 Val Val Asp Val Ile Lys Asp Gly Asp Thr Leu Cys Gly Val Ile Val  
 130 135 140  
 Glu Asn Lys Ser Gly Arg Gly Ala Ile Leu Ala Lys Arg Ile Val Asp  
 145 150 155 160  
 Cys Thr Gly Asp Ala Asp Ile Ala Ala Arg Ala Gly Ala Pro Trp Thr  
 165 170 175  
 Lys Arg Ser Lys Asp Gln Leu Met Gly Val Thr Val Met Phe Ser Cys  
 180 185 190  
 Ala Gly Val Asp Val Ala Arg Phe Asn Arg Phe Val Ala Glu Glu Leu  
 195 200 205  
 Lys Pro Thr Tyr Ala Asp Trp Gly Lys Asn Trp Thr Ile Gln Thr Thr  
 210 215 220  
 Gly Lys Glu Asp Pro Met Phe Ser Pro Tyr Met Glu Asp Ile Phe Thr  
 225 230 235 240  
 Arg Ala Gln Gln Asp Gly Val Ile Pro Gly Asp Ala Gln Ala Ile Ala  
 245 250 255  
 Gly Thr Trp Ser Thr Phe Ser Glu Ser Gly Glu Ala Phe Gln Met Asn  
 260 265 270  
 Met Val Tyr Ala Phe Gly Phe Asp Cys Thr Asp Val Phe Asp Leu Thr  
 275 280 285  
 Lys Ala Glu Ile Ala Gly Arg Gln Gln Ala Leu Trp Ala Ile Asp Ala  
 290 295 300  
 Leu Arg His Tyr Val Pro Gly Phe Glu Asn Val Arg Leu Arg Asn Phe  
 305 310 315 320  
 Gly Ala Thr Leu Gly Thr Arg Glu Ser Arg Leu Ile Glu Gly Glu Ile  
 325 330 335

Arg Ile Ala Asp Asp Tyr Val Leu Asn Gln Gly Arg Cys Ser Asp Ser  
340 345 350

Val Gly Ile Phe Pro Glu Phe Ile Asp Gly Ser Gly Tyr Leu Ile Leu  
355 360 365

Pro Thr Thr Gly Arg Phe Phe Gln Ile Pro Tyr Gly Cys Leu Val Pro  
370 375 380

Gln Lys Val Glu Asn Leu Leu Val Ala Gly Arg Cys Ile Ser Ala Gly  
385 390 395 400

Val Val Ala His Thr Ser Met Arg Asn Met Met Cys Cys Ala Val Thr  
405 410 415

Gly Glu Ala Ala Gly Thr Ala Ala Val Val Ser Leu Gln Gln Asn Cys  
420 425 430

Thr Val Arg Gln Val Ala Ile Pro Asp Leu Gln Asn Thr Leu Gln Gln  
435 440 445

Gln Gly Val Arg Leu Ala  
450

<210> 11 <211> 253 <212> PRT <213> Escherichia coli <400> 11

Met Ser Ala Lys Arg Arg Leu Leu Ile Ala Cys Thr Leu Ile Thr Ala  
1 5 10 15

Ile Tyr His Phe Pro Ala Tyr Ser Ser Leu Glu Tyr Lys Gly Thr Phe  
20 25 30

Gly Ser Ile Asn Ala Gly Tyr Ala Asp Trp Asn Ser Gly Phe Val Asn  
35 40 45

Thr His Arg Gly Glu Val Trp Lys Val Thr Ala Asp Phe Gly Val Asn  
50 55 60

Phe Lys Glu Ala Glu Phe Tyr Ser Phe Tyr Glu Ser Asn Val Leu Asn  
65 70 75 80

His Ala Val Ala Gly Arg Asn His Thr Val Ser Ala Met Thr His Val  
85 90 95

Arg Leu Phe Asp Ser Asp Met Thr Phe Phe Gly Lys Ile Tyr Gly Gln  
100 105 110

Trp Asp Asn Ser Trp Gly Asp Asp Leu Asp Met Phe Tyr Gly Phe Gly  
115 120 125

Tyr Leu Gly Trp Asn Gly Glu Trp Gly Phe Phe Lys Pro Tyr Ile Gly  
130 135 140

Leu His Asn Gln Ser Gly Asp Tyr Val Ser Ala Lys Tyr Gly Gln Thr  
145 150 155 160

Asn Gly Trp Asn Gly Tyr Val Val Gly Trp Thr Ala Val Leu Pro Phe  
165 170 175

Thr Leu Phe Asp Glu Lys Phe Val Leu Ser Asn Trp Asn Glu Ile Glu  
180 185 190

Leu Asp Arg Asn Asp Ala Tyr Thr Glu Gln Gln Phe Gly Arg Asn Gly  
195 200 205

Leu Asn Gly Gly Leu Thr Ile Ala Trp Lys Phe Tyr Pro Arg Trp Lys  
210 215 220

Ala Ser Val Thr Trp Arg Tyr Phe Asp Asn Lys Leu Gly Tyr Asp Gly  
225 230 235 240

Phe Gly Asp Gln Met Ile Tyr Met Leu Gly Tyr Asp Phe  
245 250

<210> 12 <211> 492 <212> PRT <213> Escherichia coli <400> 12

Met Ala Ser Leu Ile Gly Leu Ala Val Cys Thr Gly Asn Ala Phe Ser  
1 5 10 15

Pro Ala Leu Ala Ala Glu Ala Lys Gln Pro Asn Leu Val Ile Ile Met  
20 25 30

Ala Asp Asp Leu Gly Tyr Gly Asp Leu Ala Thr Tyr Gly His Gln Ile  
35 40 45

Val Lys Thr Pro Asn Ile Asp Arg Leu Ala Gln Glu Gly Val Lys Phe  
50 55 60

Thr Asp Tyr Tyr Ala Pro Ala Pro Leu Ser Ser Pro Ser Arg Ala Gly  
65 70 75 80

Leu Leu Thr Gly Arg Met Pro Phe Arg Thr Gly Ile Arg Ser Trp Ile  
85 90 95

Pro Ser Gly Lys Asp Val Ala Leu Gly Arg Asn Glu Leu Thr Ile Ala  
100 105 110

Asn Leu Leu Lys Ala Gln Gly Tyr Asp Thr Ala Met Met Gly Lys Leu  
115 120 125

His Leu Asn Ala Gly Gly Asp Arg Thr Asp Gln Pro Gln Ala Gln Asp  
 130 135 140

Met Gly Phe Asp Tyr Ser Leu Ala Asn Thr Ala Gly Phe Val Thr Asp  
 145 150 155 160

Ala Thr Leu Asp Asn Ala Lys Glu Arg Pro Arg Tyr Gly Met Val Tyr  
 165 170 175

Pro Thr Gly Trp Leu Arg Asn Gly Gln Pro Thr Pro Arg Ala Asp Lys  
 180 185 190

Met Ser Gly Glu Tyr Val Ser Ser Glu Val Val Asn Trp Leu Asp Asn  
 195 200 205

Lys Lys Asp Ser Lys Pro Phe Phe Leu Tyr Val Ala Phe Thr Glu Val  
 210 215 220

His Ser Pro Leu Ala Ser Pro Lys Lys Tyr Leu Asp Met Tyr Ser Gln  
 225 230 235 240

Tyr Met Ser Ala Tyr Gln Lys Gln His Pro Asp Leu Phe Tyr Gly Asp  
 245 250 255

Trp Ala Asp Lys Pro Trp Arg Gly Val Gly Glu Tyr Tyr Ala Asn Ile  
 260 265 270

Ser Tyr Leu Asp Ala Gln Val Gly Lys Val Leu Asp Lys Ile Lys Ala  
 275 280 285

Met Gly Glu Glu Asp Asn Thr Ile Val Ile Phe Thr Ser Asp Asn Gly  
 290 295 300

Pro Val Thr Arg Glu Ala Arg Lys Val Tyr Glu Leu Asn Leu Ala Gly  
 305 310 315 320

Glu Thr Asp Gly Leu Arg Gly Arg Lys Asp Asn Leu Trp Glu Gly Gly  
 325 330 335

Ile Arg Val Pro Ala Ile Ile Lys Tyr Gly Lys His Leu Pro Gln Gly  
 340 345 350

Met Val Ser Asp Thr Pro Val Tyr Gly Leu Asp Trp Met Pro Thr Leu  
 355 360 365

Ala Lys Met Met Asn Phe Lys Leu Pro Thr Asp Arg Thr Phe Asp Gly  
 370 375 380

Glu Ser Leu Val Pro Val Leu Glu Gln Lys Ala Leu Lys Arg Glu Lys  
 385 390 395 400

Pro Leu Ile Phe Gly Ile Asp Met Pro Phe Gln Asp Asp Pro Thr Asp  
405 410 415

Glu Trp Ala Ile Arg Asp Gly Asp Trp Lys Met Ile Ile Asp Arg Asn  
420 425 430

Asn Lys Pro Lys Tyr Leu Tyr Asn Leu Lys Ser Asp Arg Tyr Glu Thr  
435 440 445

Leu Asn Leu Ile Gly Lys Lys Pro Asp Ile Glu Lys Gln Met Tyr Gly  
450 455 460

Lys Phe Leu Lys Tyr Lys Thr Asp Ile Asp Asn Asp Ser Leu Met Lys  
465 470 475 480

Ala Arg Gly Asp Lys Pro Glu Ala Val Thr Trp Gly  
485 490

<210> 13 <211> 345 <212> PRT <213> Escherichia coli <400> 13

Leu Ile Ser Leu Ser Phe Ile Pro Val Met Ser Ala Leu Pro Gly Pro  
1 5 10 15

Ile Ala Lys Gly Phe Arg Asn Glu Arg Gly Phe Val Thr Thr Thr Ile  
20 25 30

Cys Ala Met Gly Glu Leu Leu Ala Glu Phe Leu Ser Arg Asn Pro His  
35 40 45

Gln Lys Phe Thr Gln Pro Gly Glu Phe Ile Gly Pro Phe Pro Ser Gly  
50 55 60

Ala Pro Ala Ile Phe Ala Ala Gln Val Ala Lys Leu Ser His Arg Ala  
65 70 75 80

Ile Phe Phe Gly Cys Val Gly Asn Asp Asp Phe Ala Arg Leu Ile Ile  
85 90 95

Glu Arg Leu Arg His Glu Gly Val Ile Thr Asp Gly Ile His Val Met  
100 105 110

Asn Asn Ala Val Thr Gly Thr Ala Phe Val Ser Tyr Gln Asn Pro Gln  
115 120 125

Gln Arg Asp Phe Val Phe Asn Ile Pro Asn Ser Ala Cys Gly Leu Phe  
130 135 140

Thr Ala Glu His Ile Asp Lys Asp Leu Leu Lys Gln Cys Asn His Leu  
145 150 155 160

His Ile Val Gly Ser Ser Leu Phe Ser Phe Arg Met Ile Asp Val Met  
165 170 175

Arg Lys Ala Ile Thr Thr Ile Lys Ser Ala Gly Gly Thr Val Ser Phe  
180 185 190

Asp Pro Asn Ile Arg Lys Glu Met Leu Ser Ile Pro Glu Met Ala Gln  
195 200 205

Ala Leu Asp Tyr Leu Ile Glu Tyr Thr Asp Ile Phe Ile Pro Ser Glu  
210 215 220

Ser Glu Leu Pro Phe Phe Ala Arg His Lys Asn Leu Ser Glu Glu Gln  
225 230 235 240

Ile Val Ser Asp Leu Leu His Gly Gly Val Lys His Val Ala Ile Lys  
245 250 255

Arg Ala Gln Arg Gly Ala Ser Tyr Tyr Lys Leu Lys Asn Gly Thr Leu  
260 265 270

His Ala Gln His Val Ala Gly His Asp Ile Glu Ile Ile Asp Pro Thr  
275 280 285

Gly Ala Gly Asp Cys Phe Gly Ala Thr Phe Ile Thr Leu Phe Leu Ser  
290 295 300

Gly Phe Pro Ala His Lys Ala Leu Gln Tyr Ala Asn Ala Ser Gly Ala  
305 310 315 320

Leu Ala Val Met Arg Gln Gly Pro Met Glu Gly Ile Ser Ser Leu Ala  
325 330 335

Asp Ile Glu Asp Phe Leu Gln Gln His  
340 345

<210> 14 <211> 192 <212> PRT <213> Escherichia coli <400> 14

Met Tyr Met Pro Gly Lys Gln Met Leu Cys Cys Ile Leu Ile Ser Ile  
1 5 10 15

Ile Ser Glu Gly Asp Met Lys Ile Phe Ile Ser Leu Phe Leu Phe Ile  
20 25 30

Ile Ser Thr Asn Ser Phe Ala Asp Asp Ile Thr His Ala Gly Val Val  
35 40 45

Arg Ile Glu Gly Leu Ile Thr Glu Lys Thr Cys Ile Ile Ser Asp Glu  
50 55 60



Ser Lys Asn Phe Thr Val Asn Met Pro Asp Val Pro Ser Ser Ser Val  
65 70 75 80

Arg Ser Ala Gly Asp Val Thr Glu Lys Val Tyr Phe Ser Ile Thr Leu  
85 90 95

Thr Arg Cys Gly Ser Asp Val Gly Asn Ala Tyr Ile Lys Phe Thr Gly  
100 105 110

Asn Thr Val Ser Glu Asp Ala Ser Leu Tyr Lys Leu Glu Asp Gly Ser  
115 120 125

Val Glu Gly Leu Ala Leu Thr Ile Phe Asp Lys Asn Lys Gly Ser Ile  
130 135 140

Ser Asn Asp Val Lys Ser Met Val Phe Ser Leu Thr Ser Ser Val Asp  
145 150 155 160

Asn Ile Leu His Phe Phe Ala Ala Tyr Lys Ala Leu Lys Asn Asn Val  
165 170 175

Gln Pro Gly Asp Ala Asn Ala Ser Val Ser Phe Ile Val Thr Tyr Asp  
180 185 190

<210> 15 <211> 201 <212> PRT <213> Escherichia coli <400> 15

Met Ile Lys Phe Arg Leu Tyr Ile Pro Pro Val Ile Leu Gly Phe Val  
1 5 10 15

Ile Val Pro Leu Leu Val Trp Pro Thr Val Ile Ala Leu Ala Val Leu  
20 25 30

Ile Phe Thr Leu Thr Phe Leu Ala Glu Ile Ile Phe Ser Phe Pro Leu  
35 40 45

Leu Val Val Arg Ile Ser Leu Gln Glu Leu Gln Leu Glu Leu Leu Val  
50 55 60

Val Tyr Ala Leu Phe Phe Ser Val Met Gly Gly Ile Gly Trp Gln Phe  
65 70 75 80

Ser Arg Arg Thr Pro Pro Glu Leu Lys Asn Arg Leu His Cys Trp Leu  
85 90 95

Val Phe Ser Pro Val Tyr Phe Trp Leu Ile Leu Ser Asn Phe Ile Leu  
100 105 110

Tyr Ile Ser Pro Glu Lys Ser Ala Leu Leu Glu Asn Ile Arg Asn Phe  
115 120 125

Phe Leu Thr Phe Val Trp Leu Pro Leu Asn Phe Ser Pro Phe Trp Pro  
 130 135 140

Gln Pro Trp Thr Asp Phe Val Gly Pro Ile Ser Ala Gln Leu Gly Phe  
 145 150 155 160

Ala Leu Gly Tyr Tyr Cys Gln Trp Arg Ser Lys Asn Arg Ser His Arg  
 165 170 175

Lys Lys Trp Gly Asp Trp Val Thr Cys Leu Ser Leu Ala Ile Leu Ala  
 180 185 190

Leu Gly Pro Leu Phe Asn Tyr Leu Gln  
 195 200

<210> 16 <211> 234 <212> PRT <213> Escherichia coli <400> 16

Met Lys Phe Asn Leu Ser Asn Leu Ser Ala Val Leu Leu Ala Ser Gly  
 1 5 10 15

Met Leu Met Ser Thr Ala Val Thr Ala Ala Pro Gly Asp Ala Thr Gln  
 20 25 30

Phe Gly Gly Ala Asp Thr Asp Trp Ser Thr Val Asp Tyr Pro Arg Leu  
 35 40 45

Thr Asp Met Asp Asp Asn Val Asp Ser Met Gly Gly Lys Ile Arg Phe  
 50 55 60

Thr Gly Arg Val Val Lys Ala Thr Cys Lys Val Ala Thr Asp Ser Lys  
 65 70 75 80

Gln Ile Glu Val Val Leu Pro Val Val Pro Ser Asn Leu Phe Thr Gly  
 85 90 95

Ile Asp Val Glu Ala Gln Gly Ala Ser Asn Gln Thr Asp Phe Asn Ile  
 100 105 110

Asn Leu Thr Glu Cys Ser Asn Thr Asp Asp Gln Lys Ile Glu Phe Arg  
 115 120 125

Phe Thr Gly Thr Ala Asp Ser Ala Asn Lys Thr Leu Ala Asn Glu Val  
 130 135 140

Glu Gly Ser Thr Asp Ala Asp Asn Ser Gly Asn Ala Gly Ala Thr Gly  
 145 150 155 160

Val Gly Ile Arg Ile Tyr Ser Lys Gly Thr Thr Asn Asn Gly Leu Ile  
 165 170 175

Asn Leu Asn Thr Thr Ala Ala Glu Gly Ser Ala Ser Thr Ala Ala Tyr  
180 185 190

Thr Ile Pro Gly Asn Ala Thr Thr His Asp Phe Ser Ala Ala Phe Thr  
195 200 205

Ala Gly Tyr Ala Gln Asn Gly Ser Thr Val Ala Pro Gly Val Val Lys  
210 215 220

Ser Thr Ala Ser Phe Val Val Leu Tyr Glu  
225 230

<210> 17 <211> 336 <212> PRT <213> Escherichia coli <400> 17

Met Arg Ile His Thr Tyr Trp Tyr Arg Arg Tyr Phe Ile Leu Leu Ile  
1 5 10 15

Ile Ile Phe Ser Asn Val Leu Ser Ser Ile Ala Asn Ala Glu Asp Met  
20 25 30

Gly Arg Glu Arg Ala Tyr Cys Tyr Pro Gly Ser Pro Ser Asn Asn Thr  
35 40 45

Thr Pro Ala Ser Phe Ser Tyr Asn Phe Gly Thr Ile Val Val Ser Asp  
50 55 60

Val Asn Lys Asn Ala Pro Gly Thr Val Leu Pro Ser Gln Ile Trp Lys  
65 70 75 80

Val Gly Thr Tyr Lys Ala Tyr Cys Asn Ser Leu Asp Asp Tyr Glu Ile  
85 90 95

Tyr Phe Ser Ala Val Ser Gly Ile Asp Pro Ser Gly Ala Ser Gly Asp  
100 105 110

His Gln Gly Ser Asp Val Phe Ile Pro Leu Thr His Glu Ile Ser Val  
115 120 125

Ser Thr His Ile Lys Leu Tyr Asn Gln Asn Gly Thr Met Thr Asp Lys  
130 135 140

Ile Val Pro Phe Glu Asn Tyr Asn Thr Asn Tyr Pro Gly Asp Arg Ser  
145 150 155 160

Lys Pro Ser Asn Trp Ala Ser Gly Thr Glu Gly Tyr Ile Lys Ile Arg  
165 170 175

Ile Asp Lys Lys Ile Ile Ser Asp Val Ser Leu Ser Asn Val Leu Leu  
180 185 190

Val Ser Leu Tyr Val Ser Gln Ile Pro Thr Glu His Gly Pro Ile Pro  
195 200 205

Val Phe Asn Ala Tyr Ile Gly Asn Leu Asn Ile Gln Val Pro Gln Gly  
210 215 220

Cys Thr Ile Asn Glu Gly Thr Ser Phe Thr Val Asn Met Pro Asp Val  
225 230 235 240

Trp Ala Ser Glu Leu Ser Arg Ala Gly Ala Gly Ala Lys Pro Ala Gly  
245 250 255

Val Thr Pro Val Ala Thr Thr Ile Pro Ile Asn Cys Thr Asn Lys Asp  
260 265 270

Thr Asp Ala Val Met Thr Leu Val Phe Asp Gly Asn Ile Ser Ala Thr  
275 280 285

Arg Asp Thr Asn Gly Lys Gln Ser Ile Ile Gln Ala Gln Asp Asn Pro  
290 295 300

Asp Val Gly Ile Met Ile Met Asp Ser Gln Gln Asn Ser Val Asp Leu  
305 310 315 320

Asn Ala Leu Ala Thr Ser Val Gly Val Pro Phe Arg Leu Val Glu Asn  
325 330 335

<210> 18 <211> 864 <212> PRT <213> Escherichia coli <400> 18

Met Asn Leu Lys Leu Lys Arg Cys Glu Tyr Trp Met Ala Ala Gln Lys  
1 5 10 15

Gln Met Lys Arg Val Val Pro Leu Leu Leu Val Ile Met Pro Ala Cys  
20 25 30

Ser Ile Ala Gly Met Arg Phe Asn Pro Ala Phe Leu Ser Gly Asp Thr  
35 40 45

Glu Ala Val Ala Asp Leu Ser Arg Phe Glu Lys Gly Met Thr Tyr Leu  
50 55 60

Pro Gly Ser Tyr Glu Val Glu Val Trp Val Asn Asp Ser Pro Leu Leu  
65 70 75 80

Ser Arg Thr Val Thr Phe Lys Ala Asp Asp Glu Asn Gln Leu Ile Pro  
85 90 95

Cys Leu Ser Leu Ala Asp Leu Leu Ser Leu Gly Ile Asn Lys Asn Ala  
100 105 110

Leu Pro Glu Gln Ala Leu Ala Ser Ser Glu Asn Ser Cys Leu Asp Leu  
 115 120 125  
 Arg Ile Trp Phe Pro Asp Val His Tyr Met Pro Glu Leu Asp Ala Gln  
 130 135 140  
 Arg Leu Lys Leu Thr Phe Pro Gln Ala Ile Ile Lys Arg Asp Ala Arg  
 145 150 155 160  
 Gly Tyr Ile Pro Pro Glu Gln Trp Asp Asn Gly Ile Thr Ala Phe Leu  
 165 170 175  
 Leu Asn Tyr Asp Phe Ser Gly Asn Asn Asp Arg Gly Asp Tyr Ser Ser  
 180 185 190  
 Asn Asn Tyr Tyr Leu Asn Leu Arg Ala Gly Ile Asn Ile Gly Ala Trp  
 195 200 205  
 Arg Phe Arg Asp Tyr Ser Thr Trp Ser Arg Gly Ser Asn Ser Ala Gly  
 210 215 220  
 Lys Leu Glu His Ile Ser Ser Thr Leu Gln Arg Val Ile Ile Pro Phe  
 225 230 235 240  
 Arg Ser Glu Leu Thr Leu Gly Asp Thr Trp Ser Ser Ser Asp Val Phe  
 245 250 255  
 Asp Ser Val Ser Ile Arg Gly Ile Lys Leu Glu Ser Asp Glu Asn Met  
 260 265 270  
 Leu Pro Asp Ser Gln Ser Gly Phe Ala Pro Thr Val Arg Gly Ile Ala  
 275 280 285  
 Lys Ser Arg Ala Gln Val Thr Ile Lys Gln Asn Gly Tyr Val Ile Tyr  
 290 295 300  
 Gln Thr Tyr Met Pro Pro Gly Pro Phe Glu Ile Ser Asp Leu Asn Pro  
 305 310 315 320  
 Thr Ser Ser Ala Gly Asp Leu Glu Val Thr Ile Lys Glu Ser Asp Asn  
 325 330 335  
 Ser Glu Thr Val Tyr Thr Val Pro Tyr Ala Ala Val Pro Ile Leu Gln  
 340 345 350  
 Arg Glu Gly His Leu Lys Tyr Ser Thr Thr Val Gly Gln Tyr Arg Ser  
 355 360 365

Asn Ser Tyr Asn Gln Lys Ser Pro Tyr Val Phe Gln Gly Glu Leu Ile  
 370 375 380

Trp Gly Leu Pro Trp Asp Ile Thr Ala Tyr Gly Gly Ala Gln Phe Ser  
 385 390 395 400

Glu Asp Tyr Arg Ala Leu Ala Leu Gly Leu Gly Leu Asn Leu Gly Val  
 405 410 415

Phe Gly Ala Thr Ser Phe Asp Val Thr Gln Ala Asn Ser Ser Leu Val  
 420 425 430

Asp Gly Ser Lys His Gln Gly Gln Ser Tyr Arg Phe Leu Tyr Ser Lys  
 435 440 445

Ser Leu Val Gln Thr Gly Thr Ala Phe His Ile Ile Gly Tyr Arg Tyr  
 450 455 460

Ser Thr Gln Gly Phe Tyr Thr Leu Ser Asp Thr Thr Tyr Gln Gln Met  
 465 470 475 480

Ser Gly Thr Val Val Asp Pro Lys Thr Leu Asp Asp Lys Asp Tyr Val  
 485 490 495

Tyr Asn Trp Asn Asp Phe Tyr Asn Leu Arg Tyr Ser Lys Arg Gly Lys  
 500 505 510

Phe Gln Ala Ser Val Ser Gln Pro Phe Gly Asn Tyr Gly Ser Met Tyr  
 515 520 525

Leu Ser Ala Ser Gln Gln Thr Tyr Trp Asn Thr Asp Lys Lys Asp Ser  
 530 535 540

Leu Tyr Gln Val Gly Tyr Asn Thr Ser Ile Lys Gly Ile Tyr Leu Asn  
 545 550 555 560

Val Ala Trp Asn Tyr Ser Lys Ser Pro Gly Thr Asn Ala Asp Lys Ile  
 565 570 575

Val Ser Leu Asn Val Ser Leu Pro Ile Ser Asn Trp Leu Ser Ser Thr  
 580 585 590

Asn Asp Gly Arg Ser Ser Ser Asn Ala Met Thr Ala Thr Tyr Gly Tyr  
 595 600 605

Ser Gln Asp Asn His Gly Gln Val Asn Gln Tyr Thr Gly Val Ser Gly  
 610 615 620

Ser Leu Leu Glu Gln His Asn Leu Ser Tyr Asn Ile Gln His Gly Phe  
 625 630 635 640

Ala Asn Gln Asp Asn Ser Ser Ser Gly Ser Val Gly Val Asn Tyr Arg  
645 650 655

Gly Ala Tyr Gly Ser Leu Asn Ser Ala Tyr Ser Tyr Asp Asn Glu Gly  
660 665 670

Asn Gln Gln Ile Asn Tyr Gly Ile Ser Gly Ala Leu Val Val His Glu  
675 680 685

Asn Gly Leu Thr Leu Ser Gln Pro Leu Gly Glu Thr Asn Val Leu Ile  
690 695 700

Lys Ala Pro Gly Ala Asn Asn Val Asp Val Gln Arg Gly Thr Gly Ile  
705 710 715 720

Ser Thr Asp Trp Arg Gly Tyr Ala Val Val Pro Tyr Ala Thr Glu Tyr  
725 730 735

Arg Arg Asn Asn Ile Ser Leu Asp Pro Met Ser Met Asn Met His Thr  
740 745 750

Glu Leu Asp Ile Thr Ser Thr Glu Val Ile Pro Gly Lys Gly Ala Leu  
755 760 765

Val Arg Ala Glu Phe Ala Ala His Ile Gly Ile Arg Gly Leu Phe Thr  
770 775 780

Val Arg Tyr Arg Asn Lys Ser Val Pro Phe Gly Ala Thr Ala Ser Ala  
785 790 795 800

Gln Ile Lys Asn Ser Ser Gln Ile Thr Gly Ile Val Gly Asp Asn Gly  
805 810 815

Gln Leu Tyr Leu Ser Gly Leu Pro Leu Glu Gly Val Ile Asn Ile Gln  
820 825 830

Trp Gly Asp Gly Val Gln Gln Lys Cys Gln Ala Asn Tyr Lys Leu Pro  
835 840 845

Glu Thr Glu Leu Asp Asn Pro Val Ser Tyr Ala Thr Leu Glu Cys Arg  
850 855 860

<210> 19 <211> 169 <212> PRT <213> Escherichia coli <400> 19

Met Gly Ala Ile Tyr Val Lys Arg Leu Ile Leu Ser Val Ala Leu Ile  
1 5 10 15

Ile Pro Ile Ala Ser Asn Ala Ser Asp Ala Leu Asn Gln Pro Ser Ser  
20 25 30

Ser Leu Asn Asp Gly Val Glu Thr Phe Phe Ile Ser Cys Phe Asp Met  
35 40 45

Pro Gln Glu Thr Thr Thr Asp Met Asp Ala Cys Gln Arg Val Gln Leu  
50 55 60

Ala Gln Val Ser Trp Val Lys Asn Lys Tyr Ser Val Ala Ala Leu Asn  
65 70 75 80

Arg Leu Lys Gln Asp Asn Lys Asp Asp Pro Gln Arg Leu Gln Glu Leu  
85 90 95

Thr Ala Ser Phe Asn Ala Glu Ser Glu Ala Trp Thr Glu Leu Ile Glu  
100 105 110

Lys Ala Ser Lys Ser Val Gln Val Asp Tyr Val Gly Gly Thr Ile Ala  
115 120 125

Gly Thr Ala Val Ala Ser Arg Gln Ile Gly Leu Leu Glu Leu Gln Ser  
130 135 140

His Asp Ile Trp Glu His Trp Leu Arg Ser Arg Gly Leu Asn Ser Ser  
145 150 155 160

Ser Phe Ala Arg Thr Lys Val Gln Ile  
165

<210> 20 <211> 713 <212> PRT <213> Escherichia coli <400> 20

Met Ala Met Phe Thr Pro Ser Phe Ser Gly Leu Lys Gly Arg Ala Leu  
1 5 10 15

Phe Ser Leu Leu Phe Ala Ala Pro Met Ile His Ala Thr Asp Ser Val  
20 25 30

Thr Thr Lys Asp Gly Glu Thr Ile Thr Val Thr Ala Asp Ala Asn Thr  
35 40 45

Ala Thr Glu Ala Thr Asp Gly Tyr Gln Pro Leu Ser Thr Ser Thr Ala  
50 55 60

Thr Leu Thr Asp Met Pro Met Leu Asp Ile Pro Gln Val Val Asn Thr  
65 70 75 80

Val Ser Asp Gln Val Leu Glu Asn Gln Asn Ala Thr Thr Leu Asp Glu  
85 90 95

Ala Leu Tyr Asn Val Ser Asn Val Val Gln Thr Asn Thr Leu Gly Gly  
100 105 110



Thr Gln Asp Ala Phe Val Arg Arg Gly Phe Gly Ala Asn Arg Asp Gly  
 115 120 125  
 Ser Ile Met Thr Asn Gly Leu Arg Thr Val Leu Pro Arg Ser Phe Asn  
 130 135 140  
 Ala Ala Thr Glu Arg Val Glu Val Leu Lys Gly Pro Ala Ser Thr Leu  
 145 150 155 160  
 Tyr Gly Ile Leu Asp Pro Gly Gly Leu Ile Asn Val Val Thr Lys Arg  
 165 170 175  
 Pro Glu Lys Thr Phe His Gly Ser Val Ser Ala Thr Ser Ser Ser Phe  
 180 185 190  
 Gly Gly Gly Thr Gly Gln Leu Asp Ile Thr Gly Pro Ile Glu Gly Thr  
 195 200 205  
 Gln Leu Ala Tyr Arg Leu Thr Gly Glu Val Gln Asp Glu Asp Tyr Trp  
 210 215 220  
 Arg Asn Phe Gly Lys Glu Arg Ser Thr Phe Ile Ala Pro Ser Leu Thr  
 225 230 235 240  
 Trp Phe Gly Asp Asn Ala Thr Val Thr Met Leu Tyr Ser His Arg Asp  
 245 250 255  
 Tyr Lys Thr Pro Phe Asp Arg Gly Thr Ile Phe Asp Leu Thr Thr Lys  
 260 265 270  
 Gln Pro Val Asn Val Asp Arg Lys Ile Arg Phe Asp Glu Pro Phe Asn  
 275 280 285  
 Ile Thr Asp Gly Gln Ser Asp Leu Ala Gln Leu Asn Ala Glu Tyr His  
 290 295 300  
 Leu Asn Ser Gln Trp Thr Ala Arg Phe Asp Tyr Ser Tyr Ser Gln Asp  
 305 310 315 320  
 Lys Tyr Ser Asp Asn Gln Ala Arg Val Thr Ala Tyr Asp Ala Thr Thr  
 325 330 335  
 Gly Thr Leu Thr Arg Arg Val Asp Ala Thr Gln Gly Ser Thr Gln Arg  
 340 345 350  
 Met His Ala Thr Arg Ala Asp Leu Gln Gly Asn Val Asp Ile Ala Gly  
 355 360 365

Phe Tyr Asn Glu Ile Leu Gly Gly Val Ser Tyr Glu Tyr Tyr Asp Leu  
 370 375 380  
 Leu Arg Thr Asp Met Ile Arg Cys Lys Lys Ala Lys Asp Phe Asn Ile  
 385 390 395 400  
 Tyr Asn Pro Val Tyr Gly Asn Thr Ser Lys Cys Thr Thr Val Ser Ala  
 405 410 415  
 Ser Asp Ser Asp Gln Thr Ile Lys Gln Glu Asn Tyr Ser Ala Tyr Ala  
 420 425 430  
 Gln Asp Ala Leu Tyr Leu Thr Asp Asn Trp Ile Ala Val Ala Gly Ile  
 435 440 445  
 Arg Tyr Gln Tyr Tyr Thr Gln Tyr Ala Gly Lys Gly Arg Pro Phe Asn  
 450 455 460  
 Val Asn Thr Asp Ser Arg Asp Glu Gln Trp Thr Pro Lys Leu Gly Leu  
 465 470 475 480  
 Val Tyr Lys Leu Thr Pro Ser Val Ser Leu Phe Ala Asn Tyr Ser Gln  
 485 490 495  
 Thr Phe Met Pro Gln Ser Ser Ile Ala Ser Tyr Ile Gly Asp Leu Pro  
 500 505 510  
 Pro Glu Ser Ser Asn Ala Tyr Glu Val Gly Ala Lys Phe Glu Leu Phe  
 515 520 525  
 Asp Gly Ile Thr Ala Asp Ile Ala Leu Phe Asp Ile His Lys Arg Asn  
 530 535 540  
 Val Leu Tyr Thr Glu Ser Ile Gly Asp Glu Thr Ile Ala Lys Thr Ala  
 545 550 555 560  
 Gly Arg Val Arg Ser Arg Gly Val Glu Val Asp Leu Ala Gly Ala Leu  
 565 570 575  
 Thr Glu Asn Ile Asn Ile Ile Ala Ser Tyr Gly Tyr Thr Asp Ala Lys  
 580 585 590  
 Val Leu Glu Asp Pro Asp Tyr Ala Gly Lys Pro Leu Pro Asn Val Pro  
 595 600 605  
 Arg His Thr Gly Ser Leu Phe Leu Thr Tyr Asp Ile His Asn Met Pro  
 610 615 620  
 Gly Asn Asn Thr Leu Thr Phe Gly Gly Gly Gly His Gly Val Ser Arg  
 625 630 635 640

Arg Ser Ala Thr Asn Gly Ala Asp Tyr Tyr Leu Pro Gly Tyr Phe Val  
645 650 655

Ala Asp Ala Phe Ala Ala Tyr Lys Met Lys Leu Gln Tyr Pro Val Thr  
660 665 670

Leu Gln Leu Asn Val Lys Asn Leu Phe Asp Lys Thr Tyr Tyr Thr Ser  
675 680 685

Ser Ile Ala Thr Asn Asn Leu Gly Asn Gln Ile Gly Asp Pro Arg Glu  
690 695 700

Val Gln Phe Thr Val Lys Met Glu Phe  
705 710

<210> 21 <211> 606 <212> PRT <213> Escherichia coli <400> 21

Met Lys Ile Ser Trp Asn Tyr Ile Phe Lys Asn Lys Trp Arg Phe His  
1 5 10 15

Ile Thr Ser Ile Ser Leu Phe Leu Ile Met Leu Ala Val Ser Ile Ala  
20 25 30

Phe Leu His Leu Arg Phe Asn Thr Leu Ser Ser Thr Asp Lys Met Arg  
35 40 45

Leu Glu Met Tyr Lys Ser Thr Leu Tyr Ser Thr Ile Glu Gln Phe Tyr  
50 55 60

Val Leu Pro Tyr Met Leu Ser Thr Asp His Ile Ile Arg Gln Ala Val  
65 70 75 80

Ile Thr Pro Asp Asp Met Thr Ser Ser Glu Leu Asn Gln Arg Ile Ala  
85 90 95

His Phe Asn Thr Gln Leu Lys Thr Ala Ala Ile Phe Ile Leu Asp Thr  
100 105 110

Gln Gly Lys Ala Ile Ala Ser Ser Asn Trp Gln Asp Pro Gly Ser Tyr  
115 120 125

Val Gly Gln Asn Tyr Ser Tyr Arg Pro Tyr Tyr Lys His Ala Met Ser  
130 135 140

Gly Leu Asn Gly Arg Phe Tyr Gly Ile Gly Ser Thr Thr Asn Thr Pro  
145 150 155 160

Gly Phe Phe Leu Ser Thr Ser Ile Lys Asp Lys Gly Lys Ile Val Gly  
165 170 175

Val Val Val Val Lys Ile Ser Leu Asn Glu Ile Glu Lys Ala Trp Ala  
 180 185 190  
 Glu Gly Pro Glu Asn Ile Ile Val Asn Asp Glu His Gly Ile Ile Phe  
 195 200 205  
 Leu Ser Ser Lys Ser Pro Trp Arg Met Arg Thr Leu Gln Pro Leu Pro  
 210 215 220  
 Val Gln Ala Lys Gln Lys Leu Gln Ser Thr Arg Gln Tyr Ser Leu Asp  
 225 230 235 240  
 Asn Leu Leu Pro Ala Asp Tyr Tyr Pro Cys Tyr Thr Val Ser Asn Phe  
 245 250 255  
 Thr Phe Leu Lys Asp Lys Lys Glu Gln Leu Cys Leu Phe Pro Gln Tyr  
 260 265 270  
 Tyr Thr Gln Gln Ile Ala Ile Pro Glu Phe Asn Trp Lys Met Thr Ile  
 275 280 285  
 Met Val Pro Leu Asp Asn Leu Tyr Trp Ser Trp Ala Ile Ser Leu Val  
 290 295 300  
 Ile Thr Leu Ile Ile Tyr Leu Leu Phe Leu Leu Phe Ile Lys Tyr Trp  
 305 310 315 320  
 Arg Met Arg Ser His Ala Gln Gln Leu Leu Thr Leu Ala Asn Glu Thr  
 325 330 335  
 Leu Glu Lys Gln Val Lys Glu Arg Thr Ser Ala Leu Glu Leu Ile Asn  
 340 345 350  
 Gln Lys Leu Ile Gln Glu Ile Lys Glu Arg Ser Gln Ala Glu Gln Val  
 355 360 365  
 Leu Gln Ile Thr Arg Ser Glu Leu Ala Glu Ser Ser Lys Leu Ala Ala  
 370 375 380  
 Leu Gly Gln Met Ala Thr Glu Ile Ala His Glu Gln Asn Gln Pro Leu  
 385 390 395 400  
 Ala Ala Ile His Ala Leu Thr Asp Asn Ala Arg Thr Met Leu Lys Lys  
 405 410 415  
 Glu Met Tyr Pro Gln Val Glu Gln Asn Leu Lys His Ile Ile Ser Val  
 420 425 430

Ile Glu Arg Met Thr Gln Leu Ile Ser Glu Leu Lys Ala Phe Ala Ser  
 435 440 445

Arg His Arg Val Pro Lys Gly Ser Ala Asp Val Ile Lys Val Met Tyr  
 450 455 460

Ser Ala Val Ala Leu Leu Asn His Ser Met Glu Lys Asn Asn Ile Glu  
 465 470 475 480

Arg Arg Ile Lys Ala Pro Ser Met Pro Leu Phe Val Asn Cys Asp Glu  
 485 490 495

Leu Gly Leu Glu Gln Ile Phe Ser Asn Leu Ile Ser Asn Ala Leu Asp  
 500 505 510

Ser Met Glu Gly Ser Ser Tyr Lys Arg Leu Asp Ile Ala Ile Arg Gln  
 515 520 525

Ala Asn Asn Lys Val Ile Ile Thr Ile Lys Asp Ser Gly Gly Gly Phe  
 530 535 540

Ala Pro Glu Val Val Asp Arg Ile Phe Glu Pro Phe Phe Thr Thr Lys  
 545 550 555 560

Arg Arg Gly Met Gly Leu Gly Leu Ala Ile Val Ser Glu Ile Val Arg  
 565 570 575

Asn Ser Asn Gly Ala Leu His Ala Ser Asn His Pro Glu Gly Gly Ala  
 580 585 590

Val Met Thr Leu Thr Trp Pro Glu Trp Gly Glu Glu His Glu  
 595 600 605

<210> 22 <211> 101 <212> PRT <213> Escherichia coli <400> 22

Val Leu Thr Pro Gln His Leu Arg Cys Val Leu Thr Cys Ser Asp Leu  
 1 5 10 15

Leu Thr Leu Leu Ser Gly Thr Val Met Ser Gln Met Pro Leu Tyr Phe  
 20 25 30

Leu Asn Thr Gln Lys Lys Leu Thr Ala His Tyr Glu Trp Leu Gln Ile  
 35 40 45

Asn Leu Thr Asp Thr Tyr Glu Leu Val Lys Arg Leu Met Pro Ile Pro  
 50 55 60

Ser Leu Asp Val Val Val Lys Val Gly Lys Leu Val Leu Pro Glu Lys  
 65 70 75 80

Gly His His Gly Phe Tyr Pro Glu Ala Gly Val Val Tyr Arg Thr Val  
85 90 95

Ala Pro Glu Asn Pro  
100

<210> 23 <211> 263 <212> PRT <213> Escherichia coli <400> 23

Met Met Lys Asn Thr Gly Tyr Ile Leu Ala Leu Cys Leu Thr Ala Ser  
1 5 10 15

Gly His Val Leu Ala His Asp Val Trp Ile Thr Gly Lys Gln Ala Glu  
20 25 30

Asn Asn Val Thr Ala Glu Ile Gly Tyr Gly His Asn Phe Pro Ser Lys  
35 40 45

Gly Thr Ile Pro Asp Arg Arg Asp Phe Phe Glu Asn Pro Arg Leu Tyr  
50 55 60

Asn Gly Lys Glu Thr Ile Thr Leu Lys Pro Ala Ser Thr Asp Tyr Val  
65 70 75 80

Tyr Lys Thr Glu Ser Ala Ser Lys Asp Asn Gly Tyr Val Leu Ser Thr  
85 90 95

Tyr Met Lys Pro Gly Tyr Trp Ser Arg Thr Ser Ser Gly Trp Lys Pro  
100 105 110

Val Ser Arg Glu Gly Arg Asn Asp Val Ala Tyr Cys Glu Phe Val Thr  
115 120 125

Lys Tyr Ala Lys Ser Phe Ile Pro Gly Glu Gln Gln Met Pro Ala Gln  
130 135 140

Leu Tyr Gln Ser Pro Thr Gly His Glu Leu Glu Ile Ile Pro Leu Ser  
145 150 155 160

Asp Ile Ser Arg Phe Ser Glu Asn Val Lys Leu Lys Val Leu Tyr Lys  
165 170 175

Thr Ser Pro Leu Ala Gly Ala Ile Met Glu Leu Asp Ser Val Ser Tyr  
180 185 190

Leu Thr Ser Ser Arg His Thr His Ala Val Glu His Lys His Pro Val  
195 200 205

His Lys Ala Glu Leu Thr Phe Val Thr Asn Glu Asp Gly Ile Val Thr  
210 215 220

Val Pro Ser Leu His Ile Gly Gln Trp Leu Ala Lys Val Gln Asn Lys  
 225 230 235 240

Lys Ser Phe Gln Asp Lys Ser Leu Cys Asp Glu Thr Val Asp Val Ala  
 245 250 255

Thr Leu Ser Phe Ser Arg Asn  
 260

<210> 24 <211> 378 <212> PRT <213> Escherichia coli <400> 24

Met Gly Lys Ile Lys Tyr Trp Leu Ile Val Gly Phe Ile Ile Leu Phe  
 1 5 10 15

Ala Ile Phe Tyr Ile Ala Ile Ser Asp Arg Asp Ser Thr Leu Ser Arg  
 20 25 30

Leu Lys Ser Ala Gly Glu Asn Gly Asp Val Glu Ala Gln Tyr Ala Leu  
 35 40 45

Gly Leu Met Tyr Leu Tyr Gly Glu Ile Leu Asp Val Asp Tyr Gln Gln  
 50 55 60

Ala Lys Ile Trp Tyr Glu Lys Ala Ala Asp Gln Asn Asp Pro Arg Ala  
 65 70 75 80

Gln Ala Lys Leu Gly Val Met Tyr Ala Asn Gly Leu Gly Val Asn Gln  
 85 90 95

Asp Tyr Gln Gln Ser Lys Leu Trp Tyr Glu Lys Ala Ala Ala Gln Asn  
 100 105 110

Asp Val Asp Ala Gln Phe Leu Leu Gly Glu Met Tyr Asp Asp Gly Leu  
 115 120 125

Gly Val Ser Gln Asp Tyr Gln His Ala Lys Met Trp Tyr Glu Lys Ala  
 130 135 140

Ala Ala Gln Asn Asp Glu Arg Ala Gln Val Asn Leu Ala Val Leu Tyr  
 145 150 155 160

Ala Lys Gly Asn Gly Val Glu Gln Asp Tyr Arg Gln Ala Lys Ser Trp  
 165 170 175

Tyr Glu Lys Ala Ala Ala Gln Asn Ser Pro Asp Ala Gln Phe Ala Leu  
 180 185 190

Gly Ile Leu Tyr Ala Asn Ala Asn Gly Val Glu Gln Asp Tyr Gln Gln  
 195 200 205

Ala Lys Asp Trp Tyr Glu Lys Ala Ala Glu Gln Asn Phe Ala Asn Ala  
210 215 220

Gln Phe Asn Leu Gly Met Leu Tyr Tyr Lys Gly Glu Gly Val Lys Gln  
225 230 235 240

Asn Phe Arg Gln Ala Arg Glu Trp Phe Glu Lys Ala Ala Ser Gln Asn  
245 250 255

Gln Pro Asn Ala Gln Tyr Asn Leu Gly Gln Ile Tyr Tyr Tyr Gly Gln  
260 265 270

Gly Val Thr Gln Ser Tyr Arg Gln Ala Lys Asp Trp Phe Glu Lys Ala  
275 280 285

Ala Glu Lys Gly His Val Asp Ala Gln Tyr Asn Leu Gly Val Ile Tyr  
290 295 300

Glu Asn Gly Glu Gly Val Ser Gln Asn Tyr Gln Gln Ala Lys Ala Trp  
305 310 315 320

Tyr Glu Lys Ala Ala Ser Gln Asn Asp Ala Gln Ala Gln Phe Glu Leu  
325 330 335

Gly Val Met Asn Glu Leu Gly Gln Gly Glu Ser Ile Asp Leu Lys Gln  
340 345 350

Ala Arg His Tyr Tyr Glu Arg Ser Cys Asn Asn Gly Leu Lys Lys Gly  
355 360 365

Cys Glu Arg Leu Lys Glu Leu Leu Tyr Lys  
370 375

<210> 25 <211> 654 <212> PRT <213> Escherichia coli <400> 25

Met Asn Val Ile Arg Thr Val Ile Cys Thr Leu Ile Ile Leu Pro Val  
1 5 10 15

Gly Leu Gln Ala Ala Thr Ser His Ser Ser Met Val Lys Asp Thr Ile  
20 25 30

Thr Ile Val Ala Thr Gly Asn Gln Asn Thr Val Phe Glu Thr Pro Ser  
35 40 45

Met Val Ser Val Val Thr Asn Asp Thr Pro Trp Ser Gln Asn Ala Val  
50 55 60

Thr Ser Ala Gly Met Leu Lys Gly Val Ala Gly Leu Ser Gln Thr Gly  
65 70 75 80



Ala Gly Arg Thr Asn Gly Gln Thr Phe Asn Leu Arg Gly Tyr Asp Lys  
85 90 95

Ser Gly Val Leu Val Leu Val Asp Gly Val Arg Gln Leu Ser Asp Met  
100 105 110

Ala Lys Ser Ser Gly Thr Tyr Leu Asp Pro Ala Leu Val Lys Arg Ile  
115 120 125

Glu Val Val Arg Gly Pro Asn Ser Ser Leu Tyr Gly Ser Gly Gly Leu  
130 135 140

Gly Gly Val Val Asp Phe Arg Thr Ala Asp Ala Ala Asp Phe Leu Pro  
145 150 155 160

Pro Gly Glu Thr Asn Gly Leu Ser Leu Trp Gly Asn Ile Ala Ser Gly  
165 170 175

Asp His Ser Thr Gly Ser Gly Leu Thr Trp Phe Gly Lys Thr Gly Lys  
180 185 190

Thr Asp Ala Leu Leu Ser Val Ile Met Arg Lys Arg Gly Asn Ile Tyr  
195 200 205

Gln Ser Asp Gly Glu His Ala Pro Asn Lys Glu Lys Pro Ala Ala Leu  
210 215 220

Phe Ala Lys Gly Ser Val Gly Ile Thr Asp Ser Asn Lys Ala Gly Ala  
225 230 235 240

Ser Leu Arg Leu Tyr Arg Asn Asn Thr Thr Glu Pro Gly Asn Ser Thr  
245 250 255

Gln Thr His Gly Asp Ser Gly Leu Arg Asp Arg Lys Thr Val Gln Asn  
260 265 270

Asp Val Gln Phe Trp Tyr Gln Tyr Ala Pro Val Asp Asn Ser Leu Ile  
275 280 285

Asn Val Lys Ser Thr Leu Tyr Leu Ser Asp Ile Thr Ile Lys Thr Asn  
290 295 300

Gly His Asn Lys Thr Ala Glu Trp Arg Asn Asn Arg Thr Ser Gly Val  
305 310 315 320

Asn Val Val Asn Arg Ser His Thr Leu Ile Phe Pro Gly Ala His Gln  
325 330 335

Leu Ser Tyr Gly Ala Glu Tyr Tyr Arg Gln Gln Gln Lys Pro Glu Gly  
340 345 350

Ser Ala Thr Leu Tyr Pro Glu Gly Asn Ile Asp Phe Thr Ser Leu Tyr  
 355 360 365  
 Phe Gln Asp Glu Met Thr Met Lys Ser Tyr Pro Val Asn Ile Ile Val  
 370 375 380  
 Gly Ser Arg Tyr Asp Arg Tyr Lys Ser Phe Asn Pro Arg Ala Gly Glu  
 385 390 395 400  
 Leu Lys Ala Glu Arg Leu Ser Pro Arg Ala Ala Ile Ser Val Ser Pro  
 405 410 415  
 Thr Asp Trp Leu Met Met Tyr Gly Ser Ile Ser Ser Ala Phe Arg Ala  
 420 425 430  
 Pro Thr Met Ala Glu Met Tyr Arg Asp Asp Val His Phe Tyr Arg Lys  
 435 440 445  
 Gly Lys Pro Asn Tyr Trp Val Pro Asn Leu Asn Leu Lys Pro Glu Asn  
 450 455 460  
 Asn Ile Thr Arg Glu Ile Gly Ala Gly Ile Gln Leu Asp Gly Leu Leu  
 465 470 475 480  
 Thr Asp Asn Asp Arg Leu Gln Leu Lys Gly Gly Tyr Phe Gly Thr Asp  
 485 490 495  
 Ala Arg Asn Tyr Ile Ala Thr Arg Val Asp Met Lys Arg Met Arg Ser  
 500 505 510  
 Tyr Ser Tyr Asn Val Ser Arg Ala Arg Ile Trp Gly Trp Asp Met Gln  
 515 520 525  
 Gly Asn Tyr Gln Ser Asp Tyr Val Asp Trp Met Leu Ser Tyr Asn Arg  
 530 535 540  
 Thr Glu Ser Met Asp Ala Ser Ser Arg Glu Trp Leu Gly Ser Gly Asn  
 545 550 555 560  
 Pro Asp Thr Leu Ile Ser Asp Ile Ser Ile Pro Val Gly His Arg Gly  
 565 570 575  
 Val Tyr Ala Gly Trp Arg Ala Glu Leu Ser Ala Ser Ala Thr His Val  
 580 585 590  
 Lys Lys Gly Asp Pro His Gln Ala Gly Tyr Thr Ile His Ser Phe Ser  
 595 600 605

Leu Ser Tyr Lys Pro Val Ser Val Lys Gly Phe Glu Ala Ser Val Thr  
610 615 620

Leu Asp Asn Ala Phe Asn Lys Leu Ala Met Asn Gly Lys Gly Val Pro  
625 630 635 640

Leu Ser Gly Arg Thr Val Ser Leu Tyr Thr Arg Tyr Gln Trp  
645 650

<210> 26 <211> 1376 <212> PRT <213> Escherichia coli <400> 26

Met Asn Lys Ile Tyr Ala Leu Lys Tyr Cys Tyr Ile Thr Asn Thr Val  
1 5 10 15

Lys Val Val Ser Glu Leu Ala Arg Arg Val Cys Lys Gly Ser Thr Arg  
20 25 30

Arg Gly Lys Arg Leu Ser Val Leu Thr Ser Leu Ala Leu Ser Ala Leu  
35 40 45

Leu Pro Thr Val Ala Gly Ala Ser Thr Val Gly Gly Asn Asn Pro Tyr  
50 55 60

Gln Thr Tyr Arg Asp Phe Ala Glu Asn Lys Gly Gln Phe Gln Ala Gly  
65 70 75 80

Ala Thr Asn Ile Pro Ile Phe Asn Asn Lys Gly Glu Leu Val Gly His  
85 90 95

Leu Asp Lys Ala Pro Met Val Asp Phe Ser Ser Val Asn Val Ser Ser  
100 105 110

Asn Pro Gly Val Ala Thr Leu Ile Asn Pro Gln Tyr Ile Ala Ser Val  
115 120 125

Lys His Asn Lys Gly Tyr Gln Ser Val Ser Phe Gly Asp Gly Gln Asn  
130 135 140

Ser Tyr His Ile Val Asp Arg Asn Glu His Ser Ser Ser Asp Leu His  
145 150 155 160

Thr Pro Arg Leu Asp Lys Leu Val Thr Glu Val Ala Pro Ala Thr Val  
165 170 175

Thr Ser Ser Ser Thr Ala Asp Ile Leu Asn Pro Ser Lys Tyr Ser Ala  
180 185 190

Phe Tyr Arg Ala Gly Ser Gly Ser Gln Tyr Ile Gln Asp Ser Gln Gly  
195 200 205

Lys Arg His Trp Val Thr Gly Gly Tyr Gly Tyr Leu Thr Gly Gly Ile  
 210 215 220  
 Leu Pro Thr Ser Phe Phe Tyr His Gly Ser Asp Gly Ile Gln Leu Tyr  
 225 230 235 240  
 Met Gly Gly Asn Ile His Asp His Ser Ile Leu Pro Ser Phe Gly Glu  
 245 250 255  
 Ala Gly Asp Ser Gly Ser Pro Leu Phe Gly Trp Asn Thr Ala Lys Gly  
 260 265 270  
 Gln Trp Glu Leu Val Gly Val Tyr Ser Gly Val Gly Gly Gly Thr Asn  
 275 280 285  
 Leu Ile Tyr Ser Leu Ile Pro Gln Ser Phe Leu Ser Gln Ile Tyr Ser  
 290 295 300  
 Glu Asp Asn Asp Ala Pro Val Phe Phe Asn Ala Ser Ser Gly Ala Pro  
 305 310 315 320  
 Leu Gln Trp Lys Phe Asp Ser Ser Thr Gly Thr Gly Ser Leu Lys Gln  
 325 330 335  
 Gly Ser Asp Glu Tyr Ala Met His Gly Gln Lys Gly Ser Asp Leu Asn  
 340 345 350  
 Ala Gly Lys Asn Leu Thr Phe Leu Gly His Asn Gly Gln Ile Asp Leu  
 355 360 365  
 Glu Asn Ser Val Thr Gln Gly Ala Gly Ser Leu Thr Phe Thr Asp Asp  
 370 375 380  
 Tyr Thr Val Thr Thr Ser Asn Gly Ser Thr Trp Thr Gly Ala Gly Ile  
 385 390 395 400  
 Ile Val Asp Lys Asp Ala Ser Val Asn Trp Gln Val Asn Gly Val Lys  
 405 410 415  
 Gly Asp Asn Leu His Lys Ile Gly Glu Gly Thr Leu Val Val Gln Gly  
 420 425 430  
 Thr Gly Val Asn Glu Gly Gly Leu Lys Val Gly Asp Gly Thr Val Val  
 435 440 445  
 Leu Asn Gln Gln Ala Asp Ser Ser Gly His Val Gln Ala Phe Ser Ser  
 450 455 460  
 Val Asn Ile Ala Ser Gly Arg Pro Thr Val Val Leu Ala Asp Asn Gln  
 465 470 475 480

Gln Val Asn Pro Asp Asn Ile Ser Trp Gly Tyr Arg Gly Gly Val Leu  
 485 490 495

Asp Val Asn Gly Asn Asp Leu Thr Phe His Lys Leu Asn Ala Ala Asp  
 500 505 510

Tyr Gly Ala Thr Leu Gly Asn Ser Ser Asp Lys Thr Ala Asn Ile Thr  
 515 520 525

Leu Asp Tyr Gln Thr Arg Pro Ala Asp Val Lys Val Asn Glu Trp Ser  
 530 535 540

Ser Ser Asn Arg Gly Thr Val Gly Ser Leu Tyr Ile Tyr Asn Asn Pro  
 545 550 555 560

Tyr Thr His Thr Val Asp Tyr Phe Ile Leu Lys Thr Ser Ser Tyr Gly  
 565 570 575

Trp Phe Pro Thr Gly Gln Val Ser Asn Glu His Trp Glu Tyr Val Gly  
 580 585 590

His Asp Gln Asn Ser Ala Gln Ala Leu Leu Ala Asn Arg Ile Asn Asn  
 595 600 605

Lys Gly Tyr Leu Tyr His Gly Lys Leu Leu Gly Asn Ile Asn Phe Ser  
 610 615 620

Asn Lys Ala Thr Pro Gly Thr Thr Gly Ala Leu Val Met Asp Gly Ser  
 625 630 635 640

Ala Asn Met Ser Gly Thr Phe Thr Gln Glu Asn Gly Arg Leu Thr Ile  
 645 650 655

Gln Gly His Pro Val Ile His Ala Ser Thr Ser Gln Ser Ile Ala Asn  
 660 665 670

Thr Val Ser Ser Leu Gly Asp Asn Ser Val Leu Thr Gln Pro Thr Ser  
 675 680 685

Phe Thr Gln Asp Asp Trp Glu Asn Arg Thr Phe Ser Phe Gly Ser Leu  
 690 695 700

Val Leu Lys Asp Thr Asp Phe Gly Leu Gly Arg Asn Ala Thr Leu Asn  
 705 710 715 720

Thr Thr Ile Gln Ala Asp Asn Ser Ser Val Thr Leu Gly Asp Ser Arg  
 725 730 735

Val Phe Ile Asp Lys Lys Asp Gly Gln Gly Thr Ala Phe Thr Leu Glu  
 740 745 750  
 Glu Gly Thr Ser Val Ala Thr Lys Asp Ala Asp Lys Ser Val Phe Asn  
 755 760 765  
 Gly Thr Val Asn Leu Asp Asn Gln Ser Val Leu Asn Ile Asn Glu Ile  
 770 775 780  
 Phe Asn Gly Gly Ile Gln Ala Asn Asn Ser Thr Val Asn Ile Ser Ser  
 785 790 795 800  
 Asp Ser Ala Val Leu Glu Asn Ser Thr Leu Thr Ser Thr Ala Leu Asn  
 805 810 815  
 Leu Asn Lys Gly Ala Asn Val Leu Ala Ser Gln Ser Phe Val Ser Asp  
 820 825 830  
 Gly Pro Val Asn Ile Ser Asp Ala Thr Leu Ser Leu Asn Ser Arg Pro  
 835 840 845  
 Asp Glu Val Ser His Thr Leu Leu Pro Val Tyr Asp Tyr Ala Gly Ser  
 850 855 860  
 Trp Asn Leu Lys Gly Asp Asp Ala Arg Leu Asn Val Gly Pro Tyr Ser  
 865 870 875 880  
 Met Leu Ser Gly Asn Ile Asn Val Gln Asp Lys Gly Thr Val Thr Leu  
 885 890 895  
 Gly Gly Glu Gly Glu Leu Ser Pro Asp Leu Thr Leu Gln Asn Gln Met  
 900 905 910  
 Leu Tyr Ser Leu Phe Asn Gly Tyr Arg Asn Thr Trp Ser Gly Ser Leu  
 915 920 925  
 Asn Ala Pro Asp Ala Thr Val Ser Met Thr Asp Thr Gln Trp Ser Met  
 930 935 940  
 Asn Gly Asn Ser Thr Ala Gly Asn Met Lys Leu Asn Arg Thr Ile Val  
 945 950 955 960  
 Gly Phe Asn Gly Gly Thr Ser Ser Phe Thr Thr Leu Thr Thr Asp Asn  
 965 970 975  
 Leu Asp Ala Val Gln Ser Ala Phe Val Met Arg Thr Asp Leu Asn Lys  
 980 985 990  
 Ala Asp Lys Leu Val Ile Asn Lys Ser Ala Thr Gly His Asp Asn Ser  
 995 1000 1005

Ile Trp Val Asn Phe Leu Lys Lys Pro Ser Asp Lys Asp Thr Leu  
 1010 1015 1020

Asp Ile Pro Leu Val Ser Ala Pro Glu Ala Thr Ala Asp Asn Leu  
 1025 1030 1035

Phe Arg Ala Ser Thr Arg Val Val Gly Phe Ser Asp Val Thr Pro  
 1040 1045 1050

Thr Leu Ser Val Arg Lys Glu Asp Gly Lys Lys Glu Trp Val Leu  
 1055 1060 1065

Asp Gly Tyr Gln Val Ala Arg Asn Asp Gly Gln Gly Lys Ala Ala  
 1070 1075 1080

Ala Thr Phe Met His Ile Ser Tyr Asn Asn Phe Ile Thr Glu Val  
 1085 1090 1095

Asn Asn Leu Asn Lys Arg Met Gly Asp Leu Arg Asp Ile Asn Gly  
 1100 1105 1110

Glu Ala Gly Thr Trp Val Arg Leu Leu Asn Gly Ser Gly Ser Ala  
 1115 1120 1125

Asp Gly Gly Phe Thr Asp His Tyr Thr Leu Leu Gln Met Gly Ala  
 1130 1135 1140

Asp Arg Lys His Glu Leu Gly Ser Met Asp Leu Phe Thr Gly Val  
 1145 1150 1155

Met Ala Thr Tyr Thr Asp Thr Asp Ala Ser Ala Gly Leu Tyr Ser  
 1160 1165 1170

Gly Lys Thr Lys Ser Trp Gly Gly Gly Phe Tyr Ala Ser Gly Leu  
 1175 1180 1185

Phe Arg Ser Gly Ala Tyr Phe Asp Leu Ile Ala Lys Tyr Ile His  
 1190 1195 1200

Asn Glu Asn Lys Tyr Asp Leu Asn Phe Ala Gly Ala Gly Lys Gln  
 1205 1210 1215

Asn Phe Arg Ser His Ser Leu Tyr Ala Gly Ala Glu Val Gly Tyr  
 1220 1225 1230

Arg Tyr His Leu Thr Asp Thr Thr Phe Val Glu Pro Gln Ala Glu  
 1235 1240 1245

Leu Val Trp Gly Arg Leu Gln Gly Gln Thr Phe Asn Trp Asn Asp  
 1250 1255 1260  
 Ser Gly Met Asp Val Ser Met Arg Arg Asn Ser Val Asn Pro Leu  
 1265 1270 1275  
 Val Gly Arg Thr Gly Val Val Ser Gly Lys Thr Phe Ser Gly Lys  
 1280 1285 1290  
 Asp Trp Ser Leu Thr Ala Arg Ala Gly Leu His Tyr Glu Phe Asp  
 1295 1300 1305  
 Leu Thr Asp Ser Ala Asp Val His Leu Lys Asp Ala Ala Gly Glu  
 1310 1315 1320  
 His Gln Ile Asn Gly Arg Lys Asp Gly Arg Met Leu Tyr Gly Val  
 1325 1330 1335  
 Gly Leu Asn Ala Arg Phe Gly Asp Asn Thr Arg Leu Gly Leu Glu  
 1340 1345 1350  
 Val Glu Arg Ser Ala Phe Gly Lys Tyr Asn Thr Asp Asp Ala Ile  
 1355 1360 1365  
 Asn Ala Asn Ile Arg Tyr Ser Phe  
 1370 1375  
 <210> 27 <211> 349 <212> PRT <213> Escherichia coli <400> 27  
 Met Ile Thr Leu Phe Arg Leu Leu Ala Ile Leu Cys Leu Phe Phe Asn  
 1 5 10 15  
 Val Ser Ala Phe Ala Val Asp Cys Tyr Gln Asp Gly Tyr Arg Gly Thr  
 20 25 30  
 Thr Leu Ile Asn Gly Asp Leu Pro Thr Phe Lys Ile Pro Glu Asn Ala  
 35 40 45  
 Gln Pro Gly Gln Lys Ile Trp Glu Ser Gly Asp Ile Asn Ile Thr Val  
 50 55 60  
 Tyr Cys Asp Asn Ala Pro Gly Trp Ser Ser Asn Asn Pro Ser Glu Asn  
 65 70 75 80  
 Val Tyr Ala Trp Ile Lys Leu Pro Gln Ile Asn Ser Ala Asp Met Leu  
 85 90 95  
 Asn Asn Pro Tyr Leu Thr Phe Gly Val Thr Tyr Asn Gly Val Asp Tyr  
 100 105 110



Glu Gly Thr Asn Glu Lys Ile Asp Thr His Ala Cys Leu Asp Lys Tyr  
 115 120 125

Glu Gln Tyr Tyr Asn Gly Tyr Tyr His Asp Pro Val Cys Asn Gly Ser  
 130 135 140

Thr Leu Gln Lys Asn Val Thr Phe Asn Ala His Phe Arg Val Tyr Val  
 145 150 155 160

Lys Phe Lys Ser Arg Pro Ala Gly Asp Gln Thr Val Asn Phe Gly Thr  
 165 170 175

Val Asn Val Leu Gln Phe Asp Gly Glu Gly Gly Ala Asn Met Ala Pro  
 180 185 190

Asn Ala Lys Asn Leu Arg Tyr Ala Ile Thr Gly Leu Asp Asn Ile Ser  
 195 200 205

Phe Leu Asp Cys Ser Val Asp Val Arg Ile Ser Pro Glu Ser Gln Ile  
 210 215 220

Val Asn Phe Gly Gln Ile Ala Ala Asn Ser Ile Ala Thr Phe Pro Pro  
 225 230 235 240

Lys Ala Ala Phe Ser Val Ser Thr Ile Lys Asp Ile Ala Ser Asp Cys  
 245 250 255

Thr Glu Gln Phe Asp Val Ala Thr Ser Phe Phe Thr Ser Asp Thr Leu  
 260 265 270

Tyr Asp Asn Thr His Leu Glu Ile Gly Asn Gly Leu Leu Met Arg Ile  
 275 280 285

Thr Asp Gln Lys Thr Gln Glu Asp Ile Lys Phe Asn Gln Phe Lys Leu  
 290 295 300

Phe Ser Thr Tyr Ile Pro Gly Gln Ser Ala Ala Met Ala Thr Arg Asp  
 305 310 315 320

Tyr Gln Ala Glu Leu Thr Gln Lys Pro Gly Glu Pro Leu Val Tyr Gly  
 325 330 335

Pro Phe Gln Lys Asp Leu Ile Val Lys Ile Asn Tyr His  
 340 345

<210> 28 <211> 840 <212> PRT <213> Escherichia coli <400> 28

Met Asn Asn Lys Asn Thr Phe Ser Arg Asp Lys Leu Ser His Ala Ile  
 1 5 10 15

Lys Asn Ala Leu Ser Gly Val Val Cys Ser Leu Leu Phe Val Leu Pro  
 20 25 30  
 Val His Ala Val Glu Phe Asn Val Asp Met Ile Asp Ala Glu Asp Arg  
 35 40 45  
 Glu Asn Ile Asp Ile Ser Arg Phe Glu Lys Lys Gly Tyr Ile Pro Pro  
 50 55 60  
 Gly Arg Tyr Leu Val Arg Val Gln Ile Asn Lys Asn Met Leu Pro Gln  
 65 70 75 80  
 Thr Leu Ile Leu Glu Trp Val Lys Ala Asp Asn Glu Ser Gly Ser Leu  
 85 90 95  
 Leu Cys Leu Thr Lys Glu Asn Leu Thr Asn Phe Gly Leu Asn Thr Glu  
 100 105 110  
 Phe Ile Glu Ser Leu Gln Asn Ile Ala Gly Ser Glu Cys Leu Asp Leu  
 115 120 125  
 Ser Gln Arg Gln Glu Leu Thr Thr Arg Leu Asp Lys Ala Thr Met Ile  
 130 135 140  
 Leu Ser Leu Ser Val Pro Gln Ala Trp Leu Lys Tyr Gln Ala Thr Asn  
 145 150 155 160  
 Trp Thr Pro Pro Glu Phe Trp Asp Thr Gly Ile Thr Gly Phe Ile Leu  
 165 170 175  
 Asp Tyr Asn Val Tyr Ala Ser Gln Tyr Ala Pro His His Gly Asp Ser  
 180 185 190  
 Thr Gln Asn Val Ser Ser Tyr Gly Thr Leu Gly Phe Asn Leu Gly Ala  
 195 200 205  
 Trp Arg Leu Arg Ser Asp Tyr Gln Tyr Asn Gln Asn Phe Ala Asp Gly  
 210 215 220  
 Arg Ser Val Asn Arg Asp Ser Glu Phe Ala Arg Thr Tyr Leu Phe Arg  
 225 230 235 240  
 Pro Ile Pro Ser Trp Ser Ser Lys Phe Thr Met Gly Gln Tyr Asp Leu  
 245 250 255  
 Ser Ser Asn Leu Tyr Asp Thr Phe His Phe Thr Gly Ala Ser Leu Glu  
 260 265 270  
 Ser Asp Glu Ser Met Leu Pro Pro Asp Leu Gln Gly Tyr Ala Pro Gln  
 275 280 285

Ile Thr Gly Ile Ala Gln Thr Asn Ala Lys Val Thr Val Ala Gln Asn  
290 295 300

Gly Arg Val Leu Tyr Gln Thr Thr Val Ala Pro Gly Pro Phe Thr Ile  
305 310 315 320

Ser Asp Leu Gly Gln Ser Phe Gln Gly Gln Leu Asp Val Thr Val Glu  
325 330 335

Glu Glu Asp Gly Arg Thr Ser Thr Phe Gln Val Gly Ser Ala Ser Ile  
340 345 350

Pro Tyr Leu Thr Arg Lys Gly Gln Val Arg Tyr Lys Thr Ser Leu Gly  
355 360 365

Lys Pro Thr Ser Val Gly His Asn Asp Ile Asn Asn Pro Phe Phe Trp  
370 375 380

Thr Ala Glu Ala Ser Trp Gly Trp Leu Asn Asn Val Ser Leu Tyr Gly  
385 390 395 400

Gly Gly Met Phe Thr Ala Asp Asp Tyr Gln Ala Ile Thr Thr Gly Ile  
405 410 415

Gly Phe Asn Leu Asn Gln Phe Gly Ser Leu Ser Phe Asp Val Thr Gly  
420 425 430

Ala Asp Ala Ser Leu Gln Gln Gln Asn Ser Gly Asn Leu Arg Gly Tyr  
435 440 445

Ser Tyr Arg Phe Asn Tyr Ala Lys His Phe Glu Ser Thr Gly Ser Gln  
450 455 460

Ile Thr Phe Ala Gly Tyr Arg Phe Ser Asp Lys Asp Tyr Val Ser Met  
465 470 475 480

Ser Glu Tyr Leu Ser Ser Arg Asn Gly Asp Glu Ser Ile Asp Asn Glu  
485 490 495

Lys Glu Ser Tyr Val Ile Ser Leu Asn Gln Tyr Phe Glu Thr Leu Glu  
500 505 510

Leu Asn Ser Tyr Leu Asn Val Thr Arg Asn Thr Tyr Trp Asp Ser Ala  
515 520 525

Ser Asn Thr Asn Tyr Ser Val Ser Val Ser Lys Asn Phe Asp Ile Gly  
530 535 540

Asp Phe Lys Gly Ile Ser Ala Ser Leu Ala Val Ser Arg Ile Arg Trp  
 545 550 555 560  
 Asp Asp Asp Glu Glu Asn Gln Tyr Tyr Phe Ser Phe Ser Leu Pro Leu  
 565 570 575  
 Gln Gln Asn Arg Asn Ile Ser Tyr Ser Met Gln Arg Thr Gly Ser Ser  
 580 585 590  
 Asn Thr Ser Gln Met Ile Ser Trp Tyr Asp Ser Ser Asp Arg Asn Asn  
 595 600 605  
 Ile Trp Asn Ile Ser Ala Ser Ala Thr Asp Asp Asn Ile Arg Asp Gly  
 610 615 620  
 Glu Pro Thr Leu Arg Gly Ser Tyr Gln His Tyr Ser Pro Trp Gly Arg  
 625 630 635 640  
 Leu Asn Ile Asn Gly Ser Val Gln Pro Asn Gln Tyr Asn Ser Val Thr  
 645 650 655  
 Ala Gly Trp Tyr Gly Ser Leu Thr Ala Thr Arg His Gly Val Ala Leu  
 660 665 670  
 His Asp Tyr Ser Tyr Gly Asp Asn Ala Arg Met Met Val Asp Thr Asp  
 675 680 685  
 Gly Ile Ser Gly Ile Glu Ile Asn Ser Asn Arg Thr Val Thr Asn Gly  
 690 695 700  
 Leu Gly Ile Ala Val Ile Pro Ser Leu Ser Asn Tyr Thr Thr Ser Met  
 705 710 715 720  
 Leu Arg Val Asn Asn Asn Asp Leu Pro Glu Gly Val Asp Val Glu Asn  
 725 730 735  
 Ser Val Ile Arg Thr Thr Leu Thr Gln Gly Ala Ile Gly Tyr Ala Lys  
 740 745 750  
 Leu Asn Ala Thr Thr Gly Tyr Gln Ile Val Gly Val Ile Arg Gln Glu  
 755 760 765  
 Asn Gly Arg Phe Pro Pro Leu Gly Val Asn Val Thr Asp Lys Ala Thr  
 770 775 780  
 Gly Lys Asp Val Gly Leu Val Ala Glu Asp Gly Phe Val Tyr Leu Ser  
 785 790 795 800  
 Gly Ile Gln Glu Asn Ser Ile Leu His Leu Thr Trp Gly Asp Asn Thr  
 805 810 815

Cys Glu Val Thr Pro Pro Asn Gln Ser Asn Ile Ser Glu Ser Ala Ile  
820 825 830

Ile Leu Pro Cys Lys Thr Val Lys  
835 840

<210> 29 <211> 169 <212> PRT <213> Escherichia coli <400> 29

Leu Met Asn Thr Lys Gln Ser Val Ala Gln Leu Ala Val Pro His Arg  
1 5 10 15

Lys Arg Leu Ser Ser Thr Met Val Val Ala Leu Leu Leu Cys Val Val  
20 25 30

Ala Gly Ala Val Met Ile Asn Ala Ala Asp Phe Pro Ala Thr Ala Ile  
35 40 45

Glu Thr Asp Pro Gly Ala Ser Ala Phe Pro Thr Phe Tyr Ala Cys Ala  
50 55 60

Leu Ile Val Leu Ala Val Leu Leu Val Ile Arg Asp Leu Leu Gln Ala  
65 70 75 80

Lys Pro Ala Ser Cys Ala Asn Ala Gln Glu Lys Pro Ala Phe Arg Lys  
85 90 95

Thr Ala Thr Gly Ile Ala Ala Thr Ala Phe Tyr Ile Val Ala Met Ser  
100 105 110

Tyr Cys Gly Tyr Leu Ile Thr Thr Pro Val Phe Leu Ile Val Ile Met  
115 120 125

Thr Leu Met Gly Tyr Arg Arg Trp Val Leu Thr Pro Gly Ile Ala Leu  
130 135 140

Leu Leu Thr Ala Ile Leu Trp Leu Leu Phe Val Glu Ala Leu Gln Val  
145 150 155 160

Pro Leu Pro Val Gly Thr Phe Phe Glu  
165

<210> 30 <211> 311 <212> PRT <213> Escherichia coli <400> 30

Met Val Leu Leu Ala Gly Ala Ala Leu Ser Ile Ala Pro Val Gln Ala  
1 5 10 15

Ala Ser Tyr Pro Thr Lys Gln Ile Glu Leu Val Val Pro Tyr Ala Ala  
20 25 30

Gly Gly Gly Thr Asp Leu Val Ala Arg Ala Phe Ala Asp Ala Ala Lys  
 35 40 45

Asn His Leu Pro Val Ser Ile Gly Val Ile Asn Lys Pro Gly Gly Gly  
 50 55 60

Gly Ala Ile Gly Leu Ser Glu Ile Ala Ala Ala Arg Pro Asn Gly Tyr  
 65 70 75 80

Lys Ile Gly Leu Gly Thr Val Glu Leu Thr Thr Leu Pro Ser Leu Gly  
 85 90 95

Met Val Arg Phe Lys Thr Ser Asp Phe Lys Pro Ile Ala Arg Leu Asn  
 100 105 110

Ala Asp Pro Ala Ala Ile Thr Val Arg Ala Asp Ala Pro Trp Asn Ser  
 115 120 125

Tyr Glu Glu Phe Met Ala Tyr Ser Lys Ala Asn Pro Gly Lys Val Arg  
 130 135 140

Ile Gly Asn Ser Gly Thr Gly Ala Ile Trp His Leu Ala Ala Ala Ala  
 145 150 155 160

Leu Glu Asp Lys Thr Gly Thr Lys Phe Ser His Val Pro Tyr Asp Gly  
 165 170 175

Ala Ala Pro Ala Ile Thr Gly Leu Leu Gly Gly His Ile Glu Ala Val  
 180 185 190

Ser Val Ser Pro Gly Glu Val Ile Asn His Val Asn Gly Gly Lys Leu  
 195 200 205

Lys Thr Leu Val Val Met Ala Asp Glu Arg Met Lys Thr Met Pro Asp  
 210 215 220

Val Pro Thr Leu Lys Glu Lys Gly Val Asp Leu Ser Ile Gly Thr Trp  
 225 230 235 240

Arg Gly Leu Ile Val Ser Gln Lys Thr Pro Gln Asp Val Val Asp Val  
 245 250 255

Leu Ala Lys Ala Ala Lys Glu Thr Ala Glu Glu Pro Ala Phe Gln Asp  
 260 265 270

Ala Leu Gln Lys Leu Asn Leu Asn Tyr Ala Trp Leu Asp Ala Ala Ser  
 275 280 285

Phe Gln Thr Gln Ile Ser Glu Gln Glu Lys Tyr Phe Asp Glu Leu Leu  
 290 295 300

Thr Arg Leu Gly Leu Lys Lys  
305 310

<210> 31 <211> 722 <212> PRT <213> Escherichia coli <400> 31

Met Leu Arg Trp Lys Arg Cys Ile Ile Leu Thr Phe Ile Ser Gly Ala  
1 5 10 15

Ala Phe Ala Ala Pro Glu Ile Asn Val Lys Gln Asn Glu Ser Leu Pro  
20 25 30

Asp Leu Gly Ser Gln Ala Ala Gln Gln Asp Glu Gln Thr Asn Lys Gly  
35 40 45

Lys Ser Leu Lys Glu Arg Gly Ala Asp Tyr Val Ile Asn Ser Ala Thr  
50 55 60

Gln Gly Phe Glu Asn Leu Thr Pro Glu Ala Leu Glu Ser Gln Ala Arg  
65 70 75 80

Ser Tyr Leu Gln Ser Gln Ile Thr Ser Thr Ala Gln Ser Tyr Ile Glu  
85 90 95

Asp Thr Leu Ser Pro Tyr Gly Lys Val Arg Leu Asn Leu Ser Ile Gly  
100 105 110

Gln Gly Gly Asp Leu Asp Gly Ser Ser Ile Asp Tyr Phe Val Pro Trp  
115 120 125

Tyr Asp Asn Gln Thr Thr Val Tyr Phe Ser Gln Phe Ser Ala Gln Arg  
130 135 140

Lys Glu Asp Arg Thr Ile Gly Asn Ile Gly Leu Gly Val Arg Tyr Asn  
145 150 155 160

Phe Asp Lys Tyr Leu Leu Gly Gly Asn Ile Phe Tyr Asp Tyr Asp Phe  
165 170 175

Thr Arg Gly His Arg Arg Leu Gly Leu Gly Ala Glu Ala Trp Thr Asp  
180 185 190

Tyr Leu Lys Phe Ser Gly Asn Tyr Tyr His Pro Leu Ser Asp Trp Lys  
195 200 205

Asp Ser Glu Asp Phe Asp Phe Tyr Glu Glu Arg Pro Ala Arg Gly Trp  
210 215 220

Asp Ile Arg Ala Glu Val Trp Leu Pro Ser Tyr Pro Gln Leu Gly Gly  
225 230 235 240

Lys Ile Val Phe Glu Gln Tyr Tyr Gly Asp Glu Val Ala Leu Phe Gly  
 245 250 255  
 Thr Asp Asn Leu Glu Lys Asp Pro Tyr Ala Val Thr Leu Gly Leu Asn  
 260 265 270  
 Tyr Gln Pro Val Pro Leu Leu Thr Val Gly Thr Asp Tyr Lys Ala Gly  
 275 280 285  
 Thr Gly Asp Asn Ser Asp Val Ser Ile Asn Ala Thr Leu Asn Tyr Gln  
 290 295 300  
 Phe Gly Val Pro Leu Lys Asp Gln Leu Asp Ser Asp Lys Val Lys Ala  
 305 310 315 320  
 Ala His Ser Leu Met Gly Ser Arg Leu Asp Phe Val Glu Arg Asn Asn  
 325 330 335  
 Phe Ile Val Leu Glu Tyr Lys Glu Lys Asp Pro Leu Asp Val Thr Leu  
 340 345 350  
 Trp Leu Lys Ala Asp Ala Thr Asn Glu His Pro Glu Cys Val Ile Lys  
 355 360 365  
 Asp Thr Pro Glu Ala Ala Val Gly Leu Glu Lys Cys Lys Trp Thr Ile  
 370 375 380  
 Asn Ala Leu Ile Asn His His Tyr Lys Ile Val Ala Ala Ser Trp Gln  
 385 390 395 400  
 Ala Lys Asn Asn Ala Ala Arg Thr Leu Val Met Pro Val Ile Lys Glu  
 405 410 415  
 Asn Thr Leu Thr Glu Gly Asn Asn Asn His Trp Asn Leu Val Leu Pro  
 420 425 430  
 Ala Trp Gln Tyr Ser Ser Asp Gln Ala Glu Gln Glu Lys Leu Asn Thr  
 435 440 445  
 Trp Arg Val Arg Leu Ala Leu Glu Asp Glu Lys Gly Asn Arg Gln Asn  
 450 455 460  
 Ser Gly Val Val Glu Ile Thr Val Gln Gln Asp Arg Lys Ile Glu Leu  
 465 470 475 480  
 Ile Val Asn Asn Ile Ala Asn Pro Glu Glu Asn Asn His Ser His Glu  
 485 490 495



Ala Ser Ala Gln Ala Asp Gly Val Asp Gly Val Val Met Asp Leu Asp  
500 505 510

Val Thr Asp Ser Phe Gly Asp Asn Thr Asp Arg Asn Gly Asp Ala Leu  
515 520 525

Pro Glu Asp Asn Leu Thr Pro Gln Leu Tyr Asp Ala Gln Asp Lys Arg  
530 535 540

Val Thr Leu Thr Asn Lys Pro Cys Ser Thr Asp Asn Pro Cys Val Phe  
545 550 555 560

Ile Ala Lys Gln Asp Lys Glu Lys Gly Thr Val Thr Leu Ser Ser Thr  
565 570 575

Leu Pro Gly Thr Tyr Arg Trp Lys Ala Lys Ala Ala Pro Tyr Asp Asp  
580 585 590

Ser Asn Tyr Val Asp Val Thr Phe Leu Gly Ala Glu Ile Gly Gly Leu  
595 600 605

Asn Ala Phe Ile Tyr Arg Val Gly Ala Ala Lys Pro Ser Asn Leu Ile  
610 615 620

Gly Lys Asp Lys Glu Pro Leu Pro Ser Thr Thr Phe Ile Asp Leu Phe  
625 630 635 640

Tyr Gly Ala Thr Thr Ile Lys Thr Val Ser Ser Ser Arg Ser Lys Asn  
645 650 655

Leu Thr Lys Arg Trp Cys Ser Thr Thr Thr Ser Gly Asn Leu Pro Ala  
660 665 670

Arg Ala Ser Met Val Ser Gly Cys Thr Gly Glu His Ser Asn Glu Asp  
675 680 685

Ile Val Ile Pro Ala Thr Asn Arg Glu Ala Ala Gln Thr Tyr Gly Ala  
690 695 700

Gln Ala Gly Asp Gly Leu Gln Gly Tyr Gly Leu Arg Val Leu Tyr Thr  
705 710 715 720

Lys Lys

<210> 32 <211> 319 <212> PRT <213> Escherichia coli <400> 32

Met Lys Gln Asp Lys Arg Arg Gly Leu Thr Arg Ile Ala Leu Ala Leu  
1 5 10 15

Ala Leu Ala Gly Tyr Cys Val Ala Pro Val Ala Leu Ala Glu Asp Ser  
 20 25 30  
 Ala Trp Val Asp Ser Gly Glu Thr Asn Ile Phe Gln Gly Thr Ile Pro  
 35 40 45  
 Trp Leu Tyr Ser Glu Gly Gly Ser Ala Thr Thr Asp Ala Asp Arg Val  
 50 55 60  
 Thr Leu Thr Ser Asp Leu Lys Gly Ala Arg Pro Gln Gly Met Lys Arg  
 65 70 75 80  
 Thr Ser Val Phe Thr Arg Val Ile Asn Ile Gly Asp Thr Glu Gly Asp  
 85 90 95  
 Val Asp Leu Gly Gly Leu Gly Asp Asn Ala Lys Thr Ile Asp Thr Ile  
 100 105 110  
 Arg Trp Met Ser Tyr Lys Asp Ala Gln Gly Gly Asp Pro Lys Glu Leu  
 115 120 125  
 Ala Thr Lys Val Thr Ser Tyr Thr Leu Thr Asp Ala Asp Arg Gly Arg  
 130 135 140  
 Tyr Ile Gly Ile Glu Ile Thr Pro Thr Thr Gln Thr Gly Thr Pro Asn  
 145 150 155 160  
 Val Gly Thr Ala Leu His Leu Tyr Asp Val Ser Thr Ala Ser Gly Gly  
 165 170 175  
 Gly Ser Asp Ser Asp Asn Val Ala Pro Gly Pro Val Val Asn Gln Asn  
 180 185 190  
 Leu Lys Val Ala Ile Phe Val Asp Gly Thr Ser Ile Asn Leu Ile Asn  
 195 200 205  
 Gly Ser Thr Pro Ile Glu Leu Gly Lys Thr Tyr Val Ala Lys Leu Tyr  
 210 215 220  
 Ser Asp Glu Asn Lys Asn Gly Lys Phe Asp Ala Gly Thr Asp Ala Asp  
 225 230 235 240  
 Val Thr Ala Asn Tyr Asp Phe Arg Trp Val Leu Ser Gly Ser Ser Gln  
 245 250 255  
 Gln Leu Gly Thr Ser Gly Gly Ile Val Asn Ser Ser Phe Asp Asn Asn  
 260 265 270  
 Asn Leu Val Ile Pro Ala Thr Asn Asp Glu Ala Arg Thr Asn Leu Asn  
 275 280 285

Gly Pro Ala Arg Asp Gly Lys Glu Ala Leu Ser Ile Pro Thr Asn Gly  
 290 295 300

Asp Gly Val Gln Gly Tyr Lys Leu His Ile Ile Tyr Lys His Lys  
 305 310 315

<210> 33 <211> 629 <212> PRT <213> Escherichia coli <400> 33

Met Lys Lys Val Leu Thr Leu Ser Leu Leu Ala Leu Cys Val Ser His  
 1 5 10 15

Ser Ala Val Ala Ala Asn Tyr Thr Phe Asn Asn Asp Asn Ile Ala Leu  
 20 25 30

Ser Phe Asp Asp Thr Asn Ser Thr Ile Val Leu Lys Asp Arg Arg Thr  
 35 40 45

Asn His Pro Ile Thr Pro Gln Glu Leu Phe Phe Leu Thr Leu Pro Asp  
 50 55 60

Glu Thr Lys Ile His Thr Ala Asp Phe Lys Ile Lys His Ile Lys Lys  
 65 70 75 80

Gln Asp Asn Ala Ile Val Ile Asp Phe Thr Arg Pro Asp Phe Asn Val  
 85 90 95

Thr Val Gln Leu Asn Leu Val Lys Gly Lys Tyr Ala Ser Ile Asp Tyr  
 100 105 110

Thr Ile Ala Ala Val Gly Gln Pro Arg Asp Val Ala Lys Ile Thr Phe  
 115 120 125

Phe Pro Thr Lys Lys Gln Phe Gln Ala Pro Tyr Val Asp Gly Ala Ile  
 130 135 140

Thr Ser Ser Pro Ile Ile Ala Asp Ser Phe Phe Ile Leu Pro Asn Lys  
 145 150 155 160

Pro Ile Val Asn Thr Tyr Ala Tyr Glu Ala Thr Thr Asn Leu Asn Val  
 165 170 175

Glu Leu Lys Thr Pro Ile Gln Pro Glu Thr Pro Val Ser Phe Thr Thr  
 180 185 190

Trp Phe Gly Thr Phe Pro Glu Thr Ser Gln Leu Arg Arg Ser Val Asn  
 195 200 205

Gln Phe Ile Asn Ala Val Arg Pro Arg Pro Tyr Lys Pro Tyr Leu His  
 210 215 220

Tyr Asn Ser Trp Met Asp Ile Gly Phe Phe Thr Pro Tyr Thr Glu Gln  
 225 230 235 240  
 Asp Val Leu Gly Arg Met Asp Glu Trp Asn Lys Glu Phe Ile Ser Gly  
 245 250 255  
 Arg Gly Val Ala Leu Asp Ala Phe Leu Leu Asp Asp Gly Trp Asp Asp  
 260 265 270  
 Leu Thr Gly Arg Trp Leu Phe Gly Pro Ala Phe Ser Asn Gly Phe Ser  
 275 280 285  
 Lys Val Arg Glu Lys Ala Asp Ser Leu His Ser Ser Val Gly Leu Trp  
 290 295 300  
 Leu Ser Pro Trp Gly Gly Tyr Asn Lys Pro Gln Arg Arg Ser Arg Phe  
 305 310 315 320  
 Ala Cys Lys Arg Val Trp Val Arg Asn Arg Gly Arg Gln Ala Gly Ala  
 325 330 335  
 Phe Gly Ser Glu Leu Leu Lys Asn Phe Asn Glu Gln Ile Ile Asn Leu  
 340 345 350  
 Ile Lys Asn Glu His Ile Thr Ser Phe Lys Leu Asp Gly Met Gly Asn  
 355 360 365  
 Ala Ser Ser His Ile Lys Gly Ser Pro Phe Ala Ser Asp Phe Asp Ala  
 370 375 380  
 Ser Ile Ala Leu Leu His Asn Met Arg Arg Ala Asn Pro Asn Leu Phe  
 385 390 395 400  
 Ile Asn Leu Thr Thr Gly Thr Asn Ala Ser Pro Ser Trp Leu Phe Tyr  
 405 410 415  
 Ala Asp Ser Ile Trp Arg Gln Gly Asp Asp Ile Asn Leu Tyr Gly Pro  
 420 425 430  
 Gly Thr Pro Val Gln Gln Trp Ile Thr Tyr Arg Asp Ala Glu Thr Tyr  
 435 440 445  
 Arg Ser Ile Val Arg Lys Gly Pro Leu Phe Pro Leu Asn Ser Leu Met  
 450 455 460  
 Tyr His Gly Ile Val Ser Ala Glu Asn Ala Tyr Tyr Gly Leu Glu Lys  
 465 470 475 480

Val Gln Thr Asp Ser Asp Phe Ala Asp Gln Val Trp Ser Tyr Phe Ala  
485 490 495

Thr Gly Thr Gln Leu Gln Glu Leu Tyr Ile Thr Pro Ser Met Leu Asn  
500 505 510

Lys Val Lys Trp Asp Thr Leu Ala Lys Ala Ala Lys Trp Ser Lys Glu  
515 520 525

Asn Ala Ser Val Leu Val Asp Thr His Trp Ile Gly Gly Asp Pro Thr  
530 535 540

Ala Leu Ala Val Tyr Gly Trp Ala Ser Trp Ser Lys Asp Lys Ala Ile  
545 550 555 560

Leu Gly Leu Arg Asn Pro Ser Asp Lys Pro Gln Thr Tyr Tyr Leu Asp  
565 570 575

Leu Ala Lys Asp Phe Glu Ile Pro Ala Gly Asn Ala Ala Gln Phe Ser  
580 585 590

Leu Lys Ala Val Tyr Gly Ser Asn Lys Thr Val Pro Val Glu Tyr Lys  
595 600 605

Asn Ala Thr Val Ile Thr Leu Gln Pro Leu Glu Thr Leu Val Phe Glu  
610 615 620

Ala Val Thr Ile Asn  
625

<210> 34 <211> 1778 <212> PRT <213> Escherichia coli <400> 34

Met Asn Lys Ile Phe Lys Val Ile Trp Asn Pro Ala Thr Gly Ser Tyr  
1 5 10 15

Thr Val Ala Ser Glu Thr Ala Lys Ser Arg Gly Lys Lys Ser Gly Arg  
20 25 30

Ser Lys Leu Leu Ile Ser Ala Leu Val Ala Gly Gly Leu Leu Ser Ser  
35 40 45

Phe Gly Ala Ser Ala Asp Asn Tyr Thr Gly Gln Pro Thr Asp Tyr Gly  
50 55 60

Asp Gly Ser Ala Gly Asp Gly Trp Val Ala Ile Gly Lys Gly Ala Lys  
65 70 75 80

Ala Asn Thr Phe Met Asn Thr Ser Gly Ala Ser Thr Ala Leu Gly Tyr  
85 90 95

Asp Ala Ile Ala Glu Gly Glu Tyr Ser Ser Ala Ile Gly Ser Lys Thr  
 100 105 110  
 Leu Ala Thr Gly Gly Ala Ser Met Ala Phe Gly Val Ser Ala Lys Ala  
 115 120 125  
 Met Gly Asp Arg Ser Val Ala Leu Gly Ala Ser Ser Val Ala Asn Gly  
 130 135 140  
 Asp Arg Ser Met Ala Phe Gly Arg Tyr Ala Lys Thr Asn Gly Phe Thr  
 145 150 155 160  
 Ser Leu Ala Ile Gly Asp Ser Ser Leu Ala Asp Gly Glu Lys Thr Ile  
 165 170 175  
 Ala Leu Gly Asn Thr Ala Lys Ala Tyr Glu Ile Met Ser Ile Ala Leu  
 180 185 190  
 Gly Asp Asn Ala Asn Ala Ser Lys Glu Tyr Ala Met Ala Leu Gly Ala  
 195 200 205  
 Ser Ser Lys Ala Gly Gly Ala Asp Ser Leu Ala Phe Gly Arg Lys Ser  
 210 215 220  
 Thr Ala Asn Ser Thr Gly Ser Leu Ala Ile Gly Ala Asp Ser Ser Ser  
 225 230 235 240  
 Ser Asn Asp Asn Ala Ile Ala Ile Gly Asn Lys Thr Gln Ala Leu Gly  
 245 250 255  
 Val Asn Ser Met Ala Leu Gly Asn Ala Ser Gln Ala Ser Gly Glu Ser  
 260 265 270  
 Ser Ile Ala Leu Gly Asn Thr Ser Glu Ala Ser Glu Gln Asn Ala Ile  
 275 280 285  
 Ala Leu Gly Gln Gly Ser Ile Ala Ser Lys Val Asn Ser Ile Ala Leu  
 290 295 300  
 Gly Ser Asn Ser Leu Ser Ser Gly Glu Asn Ala Ile Ala Leu Gly Glu  
 305 310 315 320  
 Gly Ser Ala Ala Gly Gly Ser Asn Ser Leu Ala Phe Gly Ser Gln Ser  
 325 330 335  
 Arg Ala Asn Gly Asn Asp Ser Val Ala Ile Gly Val Gly Ala Ala Ala  
 340 345 350  
 Ala Thr Asp Asn Ser Val Ala Ile Gly Ala Gly Ser Thr Thr Asp Ala  
 355 360 365

Ser Asn Thr Val Ser Val Gly Asn Ser Ala Thr Lys Arg Lys Ile Val  
370 375 380

Asn Met Ala Ala Gly Ala Ile Ser Asn Thr Ser Thr Asp Ala Ile Asn  
385 390 395 400

Gly Ser Gln Leu Tyr Thr Ile Ser Asp Ser Val Ala Lys Arg Leu Gly  
405 410 415

Gly Gly Ala Thr Val Gly Ser Asp Gly Thr Val Thr Ala Val Ser Tyr  
420 425 430

Ala Leu Arg Ser Gly Thr Tyr Asn Asn Val Gly Asp Ala Leu Ser Gly  
435 440 445

Ile Asp Asn Asn Thr Leu Gln Trp Asn Lys Thr Ala Gly Ala Phe Ser  
450 455 460

Ala Asn His Gly Ala Asn Ala Thr Asn Lys Ile Thr Asn Val Ala Lys  
465 470 475 480

Gly Thr Val Ser Ala Thr Ser Thr Asp Val Val Asn Gly Ser Gln Leu  
485 490 495

Tyr Asp Leu Gln Gln Asp Ala Leu Leu Trp Asn Gly Thr Ala Phe Ser  
500 505 510

Ala Ala His Gly Thr Glu Ala Thr Ser Lys Ile Thr Asn Val Thr Ala  
515 520 525

Gly Asn Leu Thr Ala Gly Ser Thr Asp Ala Val Asn Gly Ser Gln Leu  
530 535 540

Lys Thr Thr Asn Asp Asn Val Thr Thr Asn Thr Thr Asn Ile Ala Thr  
545 550 555 560

Asn Thr Thr Asn Ile Thr Asn Leu Thr Asp Ala Val Asn Gly Leu Gly  
565 570 575

Asp Asp Ser Leu Leu Trp Asn Lys Ala Ala Gly Ala Phe Ser Ala Ala  
580 585 590

His Gly Thr Glu Ala Thr Ser Lys Ile Thr Asn Val Thr Ala Gly Asn  
595 600 605

Leu Thr Ala Gly Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Lys Thr  
610 615 620

Thr Asn Asp Asn Val Thr Thr Asn Thr Thr Asn Ile Ala Thr Asn Thr  
 625 630 635 640

Thr Asn Ile Thr Asn Leu Thr Asp Ala Val Asn Gly Leu Gly Asp Asp  
 645 650 655

Ser Leu Leu Trp Asn Lys Thr Ala Gly Ala Phe Ser Ala Ala His Gly  
 660 665 670

Thr Asp Ala Thr Ser Lys Ile Thr Asn Val Thr Ala Gly Asn Leu Thr  
 675 680 685

Ala Gly Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Lys Thr Thr Asn  
 690 695 700

Asp Asn Val Thr Thr Asn Thr Thr Asn Ile Ala Thr Asn Thr Thr Asn  
 705 710 715 720

Ile Thr Asn Leu Thr Asp Ala Val Asn Gly Leu Gly Asp Asp Ser Leu  
 725 730 735

Leu Trp Asn Lys Thr Ala Gly Ala Phe Ser Ala Ala His Gly Thr Asp  
 740 745 750

Ala Thr Ser Lys Ile Thr Asn Val Lys Ala Gly Asp Leu Thr Ala Gly  
 755 760 765

Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Lys Thr Thr Asn Asp Asn  
 770 775 780

Val Ser Thr Asn Thr Thr Asn Ile Thr Asn Leu Thr Asp Ala Val Asn  
 785 790 795 800

Gly Leu Gly Asp Asp Ser Leu Leu Trp Asn Lys Thr Ala Gly Ala Phe  
 805 810 815

Ser Ala Ala His Gly Thr Asp Ala Thr Ser Lys Ile Thr Asn Val Lys  
 820 825 830

Ala Gly Asp Leu Thr Ala Gly Ser Thr Asp Ala Val Asn Gly Ser Gln  
 835 840 845

Leu Lys Thr Thr Asn Asp Asn Val Ser Thr Asn Thr Thr Asn Ile Thr  
 850 855 860

Asn Leu Thr Asp Ser Val Gly Asp Leu Lys Asp Asp Ser Leu Leu Trp  
 865 870 875 880

Asn Lys Ala Ala Gly Ala Phe Ser Ala Ala His Gly Thr Glu Ala Thr  
 885 890 895



Ser Lys Ile Thr Asn Leu Leu Ala Gly Lys Ile Ser Ser Asn Ser Thr  
 900 905 910

Asp Ala Ile Asn Gly Ser Gln Leu Tyr Gly Val Ala Asp Ser Phe Thr  
 915 920 925

Ser Tyr Leu Gly Gly Gly Ala Asp Ile Ser Asp Thr Gly Val Leu Ser  
 930 935 940

Gly Pro Thr Tyr Thr Ile Gly Gly Thr Asp Tyr Thr Asn Val Gly Asp  
 945 950 955 960

Ala Leu Ala Ala Ile Asn Thr Ser Phe Ser Thr Ser Leu Gly Asp Ala  
 965 970 975

Leu Leu Trp Asp Ala Thr Ala Gly Lys Phe Ser Ala Lys His Gly Ile  
 980 985 990

Asn Asn Ala Pro Ser Val Ile Thr Asp Val Ala Asn Gly Ala Val Ser  
 995 1000 1005

Ser Thr Ser Ser Asp Ala Ile Asn Gly Ser Gln Leu Tyr Gly Val  
 1010 1015 1020

Ser Asp Tyr Ile Ala Asp Ala Leu Gly Gly Asn Ala Val Val Asn  
 1025 1030 1035

Thr Asp Gly Ser Ile Thr Thr Pro Thr Tyr Ala Ile Ala Gly Gly  
 1040 1045 1050

Ser Tyr Asn Asn Val Gly Asp Ala Leu Glu Ala Ile Asp Thr Thr  
 1055 1060 1065

Leu Asp Asp Ala Leu Leu Trp Asp Thr Thr Ala Asn Gly Gly Asn  
 1070 1075 1080

Gly Ala Phe Ser Ala Ala His Gly Lys Asp Lys Thr Ala Ser Val  
 1085 1090 1095

Ile Thr Asn Val Ala Asn Gly Ala Val Ser Ala Thr Ser Asn Asp  
 1100 1105 1110

Ala Ile Asn Gly Ser Gln Leu Tyr Ser Thr Asn Lys Tyr Ile Ala  
 1115 1120 1125

Asp Ala Leu Gly Gly Asp Ala Glu Val Asn Ala Asp Gly Thr Ile  
 1130 1135 1140

Thr	Ala	Pro	Thr	Tyr	Thr	Ile	Ala	Asn	Thr	Asp	Tyr	Asn	Asn	Val
1145						1150					1155			
Gly	Glu	Ala	Leu	Asp	Ala	Leu	Asp	Asn	Asn	Ala	Leu	Leu	Trp	Asp
1160						1165					1170			
Glu	Asp	Ala	Gly	Ala	Tyr	Asn	Ala	Ser	His	Asp	Gly	Asn	Ala	Ser
1175						1180					1185			
Lys	Ile	Thr	Asn	Val	Ala	Ala	Gly	Asp	Leu	Ser	Thr	Thr	Ser	Thr
1190						1195					1200			
Asp	Ala	Val	Asn	Gly	Ser	Gln	Leu	Asn	Ala	Thr	Asn	Ile	Leu	Val
1205						1210					1215			
Thr	Gln	Asn	Ser	Gln	Met	Ile	Asn	Gln	Leu	Ala	Gly	Asn	Thr	Ser
1220						1225					1230			
Glu	Thr	Tyr	Ile	Glu	Glu	Asn	Gly	Ala	Gly	Ile	Asn	Tyr	Val	Arg
1235						1240					1245			
Thr	Asn	Asp	Ser	Gly	Leu	Ala	Phe	Asn	Asp	Ala	Ser	Ala	Ser	Gly
1250						1255					1260			
Ile	Gly	Ala	Thr	Ala	Val	Gly	Tyr	Asn	Ala	Val	Ala	Ser	His	Ala
1265						1270					1275			
Ser	Ser	Val	Ala	Ile	Gly	Gln	Asp	Ser	Ile	Ser	Glu	Val	Asp	Thr
1280						1285					1290			
Gly	Ile	Ala	Leu	Gly	Ser	Ser	Ser	Val	Ser	Ser	Arg	Val	Ile	Val
1295						1300					1305			
Lys	Gly	Thr	Arg	Asn	Thr	Ser	Val	Ser	Glu	Glu	Gly	Val	Val	Ile
1310						1315					1320			
Gly	Tyr	Asp	Thr	Thr	Asp	Gly	Glu	Leu	Leu	Gly	Ala	Leu	Ser	Ile
1325						1330					1335			
Gly	Asp	Asp	Gly	Lys	Tyr	Arg	Gln	Ile	Ile	Asn	Val	Ala	Asp	Gly
1340						1345					1350			
Ser	Glu	Ala	His	Asp	Ala	Val	Thr	Val	Arg	Gln	Leu	Gln	Asn	Ala
1355						1360					1365			
Ile	Gly	Ala	Val	Ala	Thr	Thr	Pro	Thr	Lys	Tyr	Tyr	His	Ala	Asn
1370						1375					1380			
Ser	Thr	Ala	Glu	Asp	Ser	Leu	Ala	Val	Gly	Glu	Asp	Ser	Leu	Ala
1385						1390					1395			

Met Gly 1400	Ala Lys Thr Ile Val 1405	Asn Gly Asn Ala Gly 1410	Ile Gly Ile
Gly Leu 1415	Asn Thr Leu Val Leu 1420	Ala Asp Ala Ile Asn 1425	Gly Ile Ala
Ile Gly 1430	Ser Asn Ala Arg Ala 1435	Asn His Ala Asp Ser 1440	Ile Ala Met
Gly Asn 1445	Gly Ser Gln Thr Thr 1450	Arg Gly Ala Gln Thr 1455	Asn Tyr Thr
Ala Tyr 1460	Asn Met Asp Ala Pro 1465	Gln Asn Ser Val Gly 1470	Glu Phe Ser
Val Gly 1475	Ser Glu Asp Gly Gln 1480	Arg Gln Ile Thr Asn 1485	Val Ala Ala
Gly Ser 1490	Ala Asp Thr Asp Ala 1495	Val Asn Val Gly Gln 1500	Leu Lys Val
Thr Asp 1505	Ala Gln Val Ser Gln 1510	Asn Thr Gln Ser Ile 1515	Thr Asn Leu
Asn Thr 1520	Gln Val Thr Asn Leu 1525	Asp Thr Arg Val Thr 1530	Asn Ile Glu
Asn Gly 1535	Ile Gly Asp Ile Val 1540	Thr Thr Gly Ser Thr 1545	Lys Tyr Phe
Lys Thr 1550	Asn Thr Asp Gly Ala 1555	Asp Ala Asn Ala Gln 1560	Gly Lys Asp
Ser Val 1565	Ala Ile Gly Ser Gly 1570	Ser Ile Ala Ala Ala 1575	Asp Asn Ser
Val Ala 1580	Leu Gly Thr Gly Ser 1585	Val Ala Asp Glu Glu 1590	Asn Thr Ile
Ser Val 1595	Gly Ser Ser Thr Asn 1600	Gln Arg Arg Ile Thr 1605	Asn Val Ala
Ala Gly 1610	Val Asn Ala Thr Asp 1615	Ala Val Asn Val Ser 1620	Gln Leu Lys
Ser Ser 1625	Glu Ala Gly Gly Val 1630	Arg Tyr Asp Thr Lys 1635	Ala Asp Gly

Ser Ile Asp Tyr Ser Asn Ile Thr Leu Gly Gly Gly Asn Ser Gly  
 1640 1645 1650  
 Thr Thr Arg Ile Ser Asn Val Ser Ala Gly Val Asn Asn Asn Asp  
 1655 1660 1665  
 Ala Val Asn Tyr Ala Gln Leu Lys Gln Ser Val Gln Glu Thr Lys  
 1670 1675 1680  
 Gln Tyr Thr Asp Gln Arg Met Val Glu Met Asp Asn Lys Leu Ser  
 1685 1690 1695  
 Lys Thr Glu Ser Lys Leu Ser Gly Gly Ile Ala Ser Ala Met Ala  
 1700 1705 1710  
 Met Thr Gly Leu Pro Gln Ala Tyr Thr Pro Gly Ala Ser Met Ala  
 1715 1720 1725  
 Ser Ile Gly Gly Gly Thr Tyr Asn Gly Glu Ser Ala Val Ala Leu  
 1730 1735 1740  
 Gly Val Ser Met Val Ser Ala Asn Gly Arg Trp Val Tyr Lys Leu  
 1745 1750 1755  
 Gln Gly Ser Thr Asn Ser Gln Gly Glu Tyr Ser Ala Ala Leu Gly  
 1760 1765 1770  
 Ala Gly Ile Gln Trp  
 1775  
 <210> 35 <211> 227 <212> PRT <213> Escherichia coli <400> 35  
 Met Asn Leu Lys Lys Thr Leu Leu Ser Val Leu Met Ile Leu Gln Leu  
 1 5 10 15  
 Cys Leu Leu Val Gly Cys Asp Tyr Ile Glu Lys Ala Ser Lys Val Asp  
 20 25 30  
 Asp Leu Val Thr Gln Gln Glu Leu Gln Lys Ser Lys Ile Glu Ala Leu  
 35 40 45  
 Glu Lys Gln Gln Glu Leu Asp Lys Arg Lys Ile Glu His Phe Glu Lys  
 50 55 60  
 Gln Gln Thr Thr Ile Ile Asn Ser Thr Lys Thr Leu Ala Gly Val Val  
 65 70 75 80  
 Lys Ala Val Lys Asn Lys Gln Asp Glu Phe Val Phe Thr Glu Phe Asn  
 85 90 95

Pro Ala Gln Thr Gln Tyr Phe Ile Leu Asn Asn Gly Ser Val Gly Leu  
100 105 110

Ala Gly Lys Ile Leu Ser Ile Asp Ala Val Glu Asn Gly Ser Val Ile  
115 120 125

Arg Ile Ser Leu Val Asn Leu Leu Ser Val Pro Val Ser Asn Met Gly  
130 135 140

Phe Tyr Ala Thr Trp Gly Gly Glu Lys Pro Thr Asp Ile Asn Ala Leu  
145 150 155 160

Ala Lys Trp Gln Gln Leu Leu Phe Ser Thr Ala Met Asn Ser Ser Leu  
165 170 175

Lys Leu Leu Pro Gly Gln Trp Gln Asp Ile Asn Leu Thr Leu Lys Gly  
180 185 190

Val Ser Pro Asn Asn Leu Lys Tyr Leu Lys Leu Ala Ile Asn Met Ala  
195 200 205

Asn Ile Gln Phe Asp Arg Leu Gln Pro Ala Glu Ser Pro Gln Arg Lys  
210 215 220

Asn Lys Lys  
225

<210> 36 <211> 1109 <212> PRT <213> Escherichia coli <400> 36

Met Lys Arg Val Val Arg Leu Leu Gly Val Gly Leu Leu Leu Val  
1 5 10 15

Val Leu Leu Leu Ile Leu Phe Val Leu Ala Gln Thr Thr Pro Leu Ile  
20 25 30

Ser Ala Gln Asp Glu His Ala Val Trp Leu Arg Leu Leu Ile Thr Ala  
35 40 45

Ile Val Ile Cys Leu Leu Ser Met Cys Ile Phe Phe Leu Phe Ser Phe  
50 55 60

Arg Gln Asn Glu Ala Ser Thr Ile Ser Leu Tyr Ala Gln Pro Thr Asp  
65 70 75 80

Ile Lys Glu Ile Asn Thr Glu Gln Pro Asn Tyr Ala Ser Leu Leu Thr  
85 90 95

Ile Tyr Leu Arg Asp Arg Tyr Gly Pro Phe Trp Arg Arg Lys Val Arg  
100 105 110

Leu Leu Leu Val Thr Gly Glu Pro Glu Gln Ala Glu Ala Ile Ala Pro  
 115 120 125

Gly Leu Thr Gly Gln His Trp Leu Glu Gly Asp His Thr Val Leu Ile  
 130 135 140

Tyr Gly Gly Arg Pro Thr Ala Glu Pro Asp Val Thr Leu Leu Thr Ala  
 145 150 155 160

Leu Lys Lys Leu Arg Arg Ser Arg Pro Leu Asp Gly Ile Ile Trp Ala  
 165 170 175

Leu Thr Glu Glu Gln Ser Arg Gln Thr Ala Gln Leu Asp Lys Gly Trp  
 180 185 190

Arg Gly Leu Ile Asn Gly Gly Lys Arg Leu Gly Phe Gln Ala Pro Leu  
 195 200 205

Tyr Leu Trp Gln Val Cys Asp Asp Gly Asp Tyr Gln Thr Gly Arg Pro  
 210 215 220

Leu Gln Ser Val Gly Cys Leu Leu Pro Glu Arg Cys Thr Pro Glu Gln  
 225 230 235 240

Leu Ala Val Met Leu Glu Ala Ala Ala Asp Gly Thr Gly His Val Ala  
 245 250 255

Ala Thr Asp Arg Tyr Arg Met Phe Ser Ala Ala Ser Gly Ser Tyr Pro  
 260 265 270

Cys Arg Ala Gly Tyr Cys Ser Leu Ala Asp Arg Pro Glu Thr Ala Ala  
 275 280 285

Gly Arg Arg Arg Ile Phe Phe Pro Ala Pro Ala Arg Pro Asp Val Gln  
 290 295 300

Pro Ala Ala Cys Arg Arg Ala Gly Gly Gln His Leu Met Gln Trp Leu  
 305 310 315 320

Pro Ser Pro Val Trp Ala Gly Val Thr Val Ile Thr Arg Ala Gly Ala  
 325 330 335

Arg Trp Val Phe Leu Trp Leu Arg Thr Ala Leu Met Ser Ala Val Cys  
 340 345 350

Val Leu Val Ile Trp Gly Ala Gly Met Thr Thr Ser Phe Phe Ala Asn  
 355 360 365

Arg Ala Leu Val Gln Glu Thr Gly Ile Gln Thr Ala Arg Ala Leu Asp  
 370 375 380

Thr Arg Leu Pro Leu Ala Glu Gln Leu Val Ala Leu His Thr Leu Gln  
385 390 395 400

Gly Glu Leu Glu Arg Leu Gln Tyr Arg Ile Arg Glu Gly Ala Pro Trp  
405 410 415

Tyr Gln Arg Phe Gly Leu Glu Arg Asn Gln Gln Leu Leu Ala Ala Ala  
420 425 430

Phe Pro Gly Tyr Ala Gln Ala Ala Asn Arg Leu Val Arg Asp Val Ala  
435 440 445

Val Asp His Leu Gln Gln Gln Leu Asn Ala Phe Val Ala Leu Pro Pro  
450 455 460

Asn Ser Pro Gln Arg Thr Ala Thr Gly Glu Gln Arg Tyr Lys Gln Leu  
465 470 475 480

Lys Ala Leu Leu Met Thr Ser Arg Pro Glu Lys Ala Asp Ala Ala Phe  
485 490 495

Phe Ser Thr Thr Leu Met Ala Asp Gly Leu Arg Tyr Glu Asn Ile Pro  
500 505 510

Glu Gly Val Arg Gln Ser Val Leu Pro Ser Leu Leu Thr Phe Trp Thr  
515 520 525

Ala Asn Leu Pro Glu His Pro Gln Trp Lys Thr Ser Pro Pro Pro Glu  
530 535 540

Leu Thr Gly Ala Val Arg Lys Ile Leu Leu Arg Gln Ile Gly Val Arg  
545 550 555 560

Asn Ala Glu Asn Thr Leu Tyr Gln Asn Val Leu Gln Gln Val Ser Arg  
565 570 575

Asn Tyr Ala Asp Met Thr Leu Ala Asp Met Thr Gly Asp Thr Leu Thr  
580 585 590

Glu Ser Leu Phe Ser Thr Glu Gln Thr Val Pro Gly Met Phe Thr Arg  
595 600 605

Gln Ala Trp Glu Gly Gln Val Arg Glu Ala Ile Glu Gln Val Val Thr  
610 615 620

Ala Arg Arg Glu Glu Ile Asp Trp Val Leu Ser Asp Arg Gln Gln Asp  
625 630 635 640

Thr Ser Ala Asp Ile Ser Pro Asp Thr Leu Arg Asn Arg Leu Thr Ser  
 645 650 655  
 Arg Tyr Phe Thr Asp Phe Ala Gly Ser Trp Leu Ala Phe Leu Asn Ser  
 660 665 670  
 Ile His Trp Lys Lys Glu Asp Ser Leu Ser Gly Ile Leu Asp Gln Leu  
 675 680 685  
 Thr Leu Met Ala Asp Ala Arg Gln Ser Pro Leu Ile Ala Leu Thr Asp  
 690 695 700  
 Thr Leu Ala Trp Gln Ala Ala Thr Gly Arg Glu Asn Arg Gly Leu Ser  
 705 710 715 720  
 Asp Ser Leu Ala Lys Ser Ala Gln Glu Leu Phe Asn Gly Lys Glu Lys  
 725 730 735  
 Thr Pro Gln Gln Ser Arg Glu Gly Asp Asp Val Pro Val Gly Pro Leu  
 740 745 750  
 Asp Lys Thr Phe Thr Pro Leu Leu Arg Leu Leu Gly Asp Lys Ala Gly  
 755 760 765  
 Gly Gly Asp Ser Gln Leu Ser Leu Gln Thr Tyr Leu Thr Arg Val Thr  
 770 775 780  
 Arg Val Arg Leu Lys Leu Gln Gln Val Thr Asn Ala Pro Asp Pro Gln  
 785 790 795 800  
 Glu Met Thr Gln Gln Leu Ala Gln Thr Val Leu Gln Gly Lys Thr Val  
 805 810 815  
 Asp Leu Thr Asp Thr Arg Asp Tyr Gly Arg Leu Ile Ala Ala Ser Leu  
 820 825 830  
 Gly Glu Glu Trp Ser Gly Phe Gly Gln Ala Leu Phe Val Arg Pro Val  
 835 840 845  
 Glu Gln Ser Trp Arg Gln Val Leu Thr Pro Ala Ala Asp Ser Leu Asn  
 850 855 860  
 Arg Gln Trp Gln Arg Ala Ile Val Ser His Trp Asn Gln Asp Phe Ala  
 865 870 875 880  
 Gly Arg Tyr Pro Phe Lys Ala Ser Gln Asn Asp Ala Ser Leu Pro Leu  
 885 890 895  
 Leu Ala Gln Tyr Leu Arg Asp Asp Gly Arg Ile Asn Leu Phe Ile Ala  
 900 905 910



Ala Asn Leu Ser Gly Val Leu Lys Arg Glu Gly Arg Tyr Trp Val Ala  
 915 920 925

Asp Ala Met Asn Thr Gln Gly Leu Thr Val Asn Pro Asp Phe Ile Arg  
 930 935 940

Ala Leu Asn Arg Leu Arg Asp Val Ala Asp Thr Ala Phe Ala Ser Gly  
 945 950 955 960

Asp Ala Gly Ile His Phe Glu Leu Arg Ala Lys Pro Ala Arg Asp Val  
 965 970 975

Met Lys Thr His Leu Val Ile Asp Gly Gln Glu Leu Glu Tyr Phe Asn  
 980 985 990

Gln Lys Glu Arg Trp Gln Arg Phe Asn Trp Pro Asp Glu Gln Trp Gln  
 995 1000 1005

Pro Gly Ala Ser Leu Ser Trp Thr Ser Thr Gln Ala Met Glu Arg  
 1010 1015 1020

Ile Leu Ala Asp Tyr Arg Gly Ser Trp Ser Leu Ile Arg Leu Leu  
 1025 1030 1035

Glu Gln Ala Gln Val Thr Pro Val Asp Ser Ser Thr Phe Lys Val  
 1040 1045 1050

Val Trp Lys Ala Gln Asp Gly Leu Pro Leu Asn Tyr Leu Leu Arg  
 1055 1060 1065

Val Glu Gln Gly Lys Gly Pro Leu Ala Leu Leu Glu Leu Lys Asn  
 1070 1075 1080

Phe Arg Leu Pro Gly Gln Val Phe Leu Thr Gly Lys Ser Met Lys  
 1085 1090 1095

Asp Val Glu Glu Tyr Gly Glu Asp Ala Asp Glu  
 1100 1105

<210> 37 <211> 178 <212> PRT <213> Escherichia coli <400> 37

Met Phe Pro Ile Arg Phe Lys Arg Pro Ala Leu Leu Cys Met Ala Met  
 1 5 10 15

Leu Thr Val Val Leu Ser Gly Cys Gly Leu Ile Gln Lys Val Val Asp  
 20 25 30

Glu Ser Lys Ser Val Ala Ser Ala Val Phe Tyr Lys Gln Ile Lys Ile  
 35 40 45

Leu His Leu Asp Phe Phe Ser Arg Ser Ala Leu Asn Thr Asp Ala Glu  
50 55 60

Asp Thr Pro Leu Ser Thr Met Val His Val Trp Gln Leu Lys Thr Arg  
65 70 75 80

Glu Asp Phe Asp Lys Ala Asp Tyr Asp Thr Leu Phe Met Gln Glu Glu  
85 90 95

Lys Thr Leu Glu Lys Asp Val Leu Ala Lys His Thr Val Trp Val Lys  
100 105 110

Pro Glu Gly Thr Ala Ser Leu Asn Val Pro Leu Asp Lys Glu Thr Gln  
115 120 125

Phe Val Ala Ile Ile Gly Gln Phe Tyr His Pro Asp Glu Lys Ser Asp  
130 135 140

Ser Trp Arg Leu Val Ile Lys Arg Asp Glu Leu Glu Ala Asp Lys Pro  
145 150 155 160

Arg Ser Ile Glu Leu Met Arg Ser Asp Leu Arg Leu Leu Pro Leu Lys  
165 170 175

Asp Lys

<210> 38 <211> 280 <212> PRT <213> Escherichia coli <400> 38

Met Ile Ser Gly Gly Asn Met Leu Lys Glu Trp Met Ile Phe Thr Cys  
1 5 10 15

Ser Leu Leu Thr Leu Ala Gly Ala Ser Leu Pro Leu Ser Gly Cys Ile  
20 25 30

Ser Arg Gly Gln Glu Ser Ile Ser Glu Gly Ala Ala Phe Gly Ala Gly  
35 40 45

Ile Leu Arg Glu Pro Gly Ala Thr Lys Lys Ala Asp Thr Lys Asp Leu  
50 55 60

Asn Val Pro Pro Pro Val Tyr Gly Pro Pro Gln Val Ile Phe Arg Ile  
65 70 75 80

Asp Asp Asn Arg Tyr Phe Thr Leu Glu Asn Tyr Thr His Cys Glu Asn  
85 90 95

Gly Gln Thr Phe Tyr Asn Asn Lys Ala Lys Asn Ile His Val Lys Ile  
100 105 110

Leu Asp Ala Ser Gly Tyr Leu Phe Lys Gly Arg Leu Phe Trp Leu Ser  
115 120 125

Thr Arg Asp Asp Phe Leu Ala Phe Pro Ala Thr Leu Asn Thr Arg His  
130 135 140

Ala Ser Cys Met Gly Ser Asn Lys Gly Cys Met Asn Ala Val Ile Val  
145 150 155 160

Thr Thr Asp Gly Gly Lys Arg Arg Ser Gly Val Pro Tyr Gly Ser Tyr  
165 170 175

Thr Gln Asn Pro Thr Gly Ala Thr Arg Asp Tyr Asp Met Leu Val Met  
180 185 190

Asn Asp Gly Phe Tyr Leu Leu Arg Tyr Arg Gly Gly Gln Gly Arg Phe  
195 200 205

Ser Pro Val Ile Leu Arg Trp Ile Leu Ser Thr Glu Asp Ser Ser Gly  
210 215 220

Val Val Arg Ser Glu Asp Ala Tyr Glu Leu Phe Arg Pro Gly Glu Glu  
225 230 235 240

Val Pro Ser Thr Gly Phe Tyr Lys Ile Asp Leu Ser Arg Phe Tyr Pro  
245 250 255

Lys Asn Asn Val Met Glu Met Gln Cys Asp Arg Thr Leu Glu Pro Val  
260 265 270

Gln Pro Ser Glu Ser Lys Ile Gln  
275 280

<210> 39 <211> 501 <212> PRT <213> Escherichia coli <400> 39

Met Glu His Val Ser Ile Lys Thr Leu Tyr His Leu Leu Cys Cys Met  
1 5 10 15

Leu Leu Phe Ile Ser Ala Met Cys Ala Leu Ala Gln Glu His Glu Pro  
20 25 30

Ile Gly Ala Gln Asp Glu Arg Leu Ser Thr Leu Ile His Gln Arg Met  
35 40 45

Gln Glu Ala Lys Val Pro Ala Leu Ser Val Ser Val Thr Ile Lys Gly  
50 55 60

Val Arg Gln Arg Phe Val Tyr Gly Val Ala Asp Val Ala Ser Gln Lys  
65 70 75 80

Ala Asn Thr Leu Asp Thr Val Tyr Glu Leu Gly Ser Met Ser Lys Ala  
85 90 95

Phe Thr Gly Leu Val Val Gln Ile Leu Ile Gln Glu Gly Arg Leu Arg  
100 105 110

Gln Gly Asp Asp Ile Ile Thr Tyr Leu Pro Glu Met Arg Leu Asn Tyr  
115 120 125

Gln Gly Lys Pro Ala Ser Leu Thr Val Ala Asp Phe Leu Tyr His Thr  
130 135 140

Ser Gly Leu Pro Phe Ser Thr Leu Ala Arg Leu Glu Asn Pro Met Pro  
145 150 155 160

Gly Ser Ala Val Ala Gln Gln Leu Arg Asn Glu Asn Leu Leu Phe Ala  
165 170 175

Pro Gly Ala Lys Phe Ser Tyr Ala Ser Ala Asn Tyr Asp Val Leu Gly  
180 185 190

Ala Val Ile Glu Asn Val Thr Gly Lys Thr Phe Thr Glu Val Ile Ala  
195 200 205

Glu Arg Leu Thr Gln Pro Leu Gly Met Ser Ala Thr Val Ala Val Lys  
210 215 220

Gly Asp Glu Ile Ile Val Asn Lys Ala Ser Gly Tyr Lys Leu Gly Phe  
225 230 235 240

Gly Lys Pro Val Leu Phe His Ala Pro Leu Ala Arg Asn His Val Pro  
245 250 255

Ala Ala Tyr Ile His Ser Thr Leu Pro Asp Met Glu Ile Trp Ile Asp  
260 265 270

Ala Trp Leu His Arg Lys Ala Leu Pro Ala Thr Leu Arg Glu Ala Met  
275 280 285

Ser Asn Ser Trp Arg Gly Asn Ser Asp Val Pro Leu Ala Ala Asp Asn  
290 295 300

Arg Ile Leu Tyr Ala Ser Gly Trp Phe Ile Asp Gln Asn Gln Gly Pro  
305 310 315 320

Tyr Ile Ser His Gly Gly Gln Asn Pro Asn Phe Ser Ser Cys Ile Ala  
325 330 335

Leu Arg Pro Asp Gln Gln Ile Gly Ile Val Ala Leu Ala Asn Met Asn  
340 345 350

Ser Asn Leu Ile Leu Gln Leu Cys Ala Asp Ile Asp Asn Tyr Leu Arg  
355 360 365

Ile Gly Lys Tyr Ala Asp Gly Ala Gly Asp Ala Ile Thr Ala Thr Asp  
370 375 380

Thr Leu Phe Val Tyr Leu Thr Leu Leu Leu Cys Phe Trp Gly Ala Val  
385 390 395 400

Val Val Val Arg Gly Ala Phe Arg Val Tyr Arg Ala Thr Ala His Gly  
405 410 415

Pro Gly Lys Gln Gln Arg Leu Arg Leu Arg Val Arg Asp Tyr Ile Ile  
420 425 430

Ala Leu Ala Val Pro Gly Leu Val Ala Ala Met Leu Tyr Val Ala Pro  
435 440 445

Gly Ile Leu Ser Pro Gly Leu Asp Trp Arg Phe Ile Leu Val Trp Gly  
450 455 460

Pro Ser Ser Val Leu Ala Ile Pro Phe Gly Ile Ile Leu Leu Ala Phe  
465 470 475 480

Val Leu Thr Leu Asn His Gln Ile Lys Arg Ile Leu Leu His Asn Lys  
485 490 495

Glu Trp Asp Asp Glu  
500

<210> 40 <211> 682 <212> PRT <213> Escherichia coli <400> 40

Met Lys Asn Lys Tyr Ile Ile Ala Pro Gly Ile Ala Val Met Cys Ser  
1 5 10 15

Ala Val Ile Ser Ser Gly Tyr Ala Ser Ser Asp Lys Lys Glu Asp Thr  
20 25 30

Leu Val Val Thr Ala Ser Gly Phe Thr Gln Gln Leu Arg Asn Ala Pro  
35 40 45

Ala Ser Val Ser Val Ile Thr Ser Glu Gln Leu Gln Lys Lys Pro Val  
50 55 60

Ser Asp Leu Val Asp Ala Val Lys Asp Val Glu Gly Ile Ser Ile Thr  
65 70 75 80

Gly Gly Asn Glu Lys Pro Asp Ile Ser Ile Arg Gly Leu Ser Gly Asp  
                     85                    90                    95

Tyr Thr Leu Ile Leu Val Asp Gly Arg Arg Gln Ser Gly Arg Glu Ser  
                     100                    105                    110

Arg Pro Asn Gly Ser Gly Gly Phe Glu Ala Gly Phe Ile Pro Pro Val  
                     115                    120                    125

Glu Ala Ile Glu Arg Ile Glu Val Ile Arg Gly Pro Met Ser Ser Leu  
                     130                    135                    140

Tyr Gly Ser Asp Ala Ile Gly Gly Val Ile Asn Ile Ile Thr Lys Pro  
 145                    150                    155                    160

Val Asn Asn Gln Thr Trp Asp Gly Val Leu Gly Leu Gly Gly Ile Ile  
                     165                    170                    175

Gln Glu His Gly Lys Phe Gly Asn Ser Thr Thr Asn Asp Phe Tyr Leu  
                     180                    185                    190

Ser Gly Pro Leu Ile Lys Asp Lys Leu Gly Leu Gln Leu Tyr Gly Gly  
                     195                    200                    205

Met Asn Tyr Arg Lys Glu Asp Ser Ile Ser Gln Gly Thr Pro Ala Lys  
                     210                    215                    220

Asp Asn Lys Asn Ile Thr Ala Thr Leu Gln Phe Thr Pro Thr Glu Ser  
 225                    230                    235                    240

Gln Lys Phe Val Phe Glu Tyr Gly Lys Asn Asn Gln Val His Thr Leu  
                     245                    250                    255

Thr Pro Gly Glu Ser Leu Asp Ala Trp Thr Met Arg Gly Asn Leu Lys  
                     260                    265                    270

Gln Pro Asn Ser Lys Arg Glu Thr His Asn Ser Arg Ser His Trp Val  
                     275                    280                    285

Ala Ala Trp Asn Ala Gln Gly Glu Ile Leu His Pro Glu Ile Ala Val  
                     290                    295                    300

Tyr Gln Glu Lys Val Ile Arg Glu Val Lys Ser Gly Lys Lys Asp Lys  
 305                    310                    315                    320

Tyr Asn His Trp Asp Leu Asn Tyr Glu Ser Arg Lys Pro Glu Ile Thr  
                     325                    330                    335

Asn Thr Ile Ile Asp Ala Lys Val Thr Ala Phe Leu Pro Glu Asn Val  
                     340                    345                    350

Leu Thr Ile Gly Gly Gln Phe Gln His Ala Glu Leu Arg Asp Asp Ser  
 355 360 365  
 Ala Thr Gly Lys Lys Thr Thr Glu Thr Gln Ser Val Ser Ile Lys Gln  
 370 375 380  
 Lys Ala Val Phe Ile Glu Asn Glu Tyr Ala Ala Thr Asp Ser Leu Ala  
 385 390 395 400  
 Leu Thr Gly Gly Leu Arg Leu Asp Asn His Glu Ile Tyr Gly Ser Tyr  
 405 410 415  
 Trp Asn Pro Arg Leu Tyr Ala Val Tyr Asn Leu Thr Asp Asn Leu Thr  
 420 425 430  
 Leu Lys Gly Gly Ile Ala Lys Ala Phe Arg Ala Pro Ser Ile Arg Glu  
 435 440 445  
 Val Ser Pro Gly Phe Gly Thr Leu Thr Gln Gly Gly Ala Ser Ile Met  
 450 455 460  
 Tyr Gly Asn Arg Asp Leu Lys Pro Glu Thr Ser Val Thr Glu Glu Ile  
 465 470 475 480  
 Gly Ile Ile Tyr Ser Asn Asp Ser Gly Phe Ser Ala Ser Ala Thr Leu  
 485 490 495  
 Phe Asn Thr Asp Phe Lys Asn Lys Leu Thr Ser Tyr Asp Ile Gly Thr  
 500 505 510  
 Lys Asp Pro Val Thr Gly Leu Asn Thr Phe Ile Tyr Asp Asn Val Gly  
 515 520 525  
 Glu Ala Asn Ile Arg Gly Val Glu Leu Ala Thr Gln Ile Pro Val Tyr  
 530 535 540  
 Asp Lys Trp His Val Ser Ala Asn Tyr Thr Phe Thr Asp Ser Arg Arg  
 545 550 555 560  
 Lys Ser Asp Asp Glu Ser Leu Asn Gly Lys Ser Leu Lys Gly Glu Pro  
 565 570 575  
 Leu Glu Arg Thr Pro Arg His Ala Ala Asn Ala Lys Leu Glu Trp Asp  
 580 585 590  
 Tyr Thr Gln Asp Ile Thr Phe Tyr Ser Ser Leu Asn Tyr Thr Gly Lys  
 595 600 605

Gln Ile Trp Ala Ala Gln Arg Asn Gly Ala Lys Val Pro Arg Val Arg  
 610 615 620

Asn Gly Phe Thr Ser Met Asp Ile Gly Leu Asn Tyr Gln Ile Leu Pro  
 625 630 635 640

Asp Thr Leu Ile Asn Phe Ala Val Leu Asn Val Thr Asp Arg Lys Ser  
 645 650 655

Glu Asp Ile Asp Thr Ile Asp Gly Asn Trp Gln Val Asp Glu Gly Arg  
 660 665 670

Arg Tyr Trp Ala Asn Val Arg Val Ser Phe  
 675 680

<210> 41 <211> 164 <212> PRT <213> Escherichia coli <400> 41

Met Gly Phe Arg Lys Thr Ile Ile Thr Ser Val Gly Leu Ile Phe Ile  
 1 5 10 15

Ser Phe Ser Phe Val Ala Lys Cys Ser Gln Leu Lys Asn Leu Asn Asn  
 20 25 30

Tyr Ser Val Met Leu Cys Gly Lys Val Ser Asn Asn Ile Leu Asp Asp  
 35 40 45

Ile Gly Gly Tyr Lys Glu Arg Asn Ile Leu Met Leu Arg Ala Ile Lys  
 50 55 60

Lys Ile Ile Ile Met Thr Ile Val Asn Ile Ile Phe Phe Tyr Ser Phe  
 65 70 75 80

Gln Ser Thr Ala Asp Glu Met Val Leu Ile Lys Lys Tyr Gly Phe Gly  
 85 90 95

Leu Glu Arg Asp Ile Lys Gly Arg Pro Leu Ile Tyr Pro Ile Glu Asn  
 100 105 110

Tyr Asp Glu Cys Lys Lys Lys Cys Asn His Met Asn Tyr Ile Ala Asp  
 115 120 125

Val Asn Ala Gln Leu Ala Met Ser Lys Lys Asn Asn Arg Ile Phe Ala  
 130 135 140

Asn Ile Thr Phe Thr Asn Asn Ser Ser Thr Thr Tyr Phe Phe Leu Asn  
 145 150 155 160

Ile Ile Tyr Leu



<210> 42 <211> 218 <212> PRT <213> Escherichia coli <400> 42

Met Asn Gln Ile Lys Asp Asn Lys Val Ile Met Lys Ile Lys Asn Leu  
1 5 10 15

Ile Ser Val Ile Leu Leu Ser Gly Gly Ile Met Gly Thr Gly Leu Tyr  
20 25 30

Ser Ser Asp Asn His Gln Lys Ile Arg Ser Arg Phe Asn Ile Gln Glu  
35 40 45

Ser Tyr Cys Ala Ile Lys Thr Asn Gly Val Leu Gly Phe Ser Asn Arg  
50 55 60

Lys Asp Val Leu Arg Glu Asn Gly Asp Ser Thr Gly Thr Thr Ser Ser  
65 70 75 80

Ser Thr Asn Ala Met Met Leu Met Glu Asn Gly Glu Asn Glu Ile Ser  
85 90 95

Leu Glu Ile Gly Ala Leu Arg Trp Phe Ser Asp Lys Pro Ala Ser Thr  
100 105 110

Glu Glu Arg Gly His Phe Ser Gln Lys Ala Gly Cys Ser Leu Asp Leu  
115 120 125

Val Arg Phe Val Lys Gln Glu Glu Thr Ile Leu Ser Ser Ile Lys Val  
130 135 140

Thr Ile Asn Gln Gln Gly Ile Pro Glu Ala Gln Pro Asp Ser Met His  
145 150 155 160

Pro Val Ile Arg Lys Glu Ile Leu Ala Glu Gln Ala Glu Pro Gly Phe  
165 170 175

Ile Asp Pro Asp Tyr Phe Asn Glu Thr Tyr Phe Pro Lys Gly Met Lys  
180 185 190

Val Tyr Gln Phe Thr Gln Lys Val Ser Val Ala Gly Leu Pro Asp Gly  
195 200 205

Pro Gly Arg Ser Thr Pro Phe Thr Gly Ala  
210 215

<210> 43 <211> 2732 <212> PRT <213> Escherichia coli <400> 43

Met His Gln Pro Pro Val Arg Phe Thr Tyr Arg Leu Leu Ser Tyr Leu  
1 5 10 15

Val Ser Ala Ile Ile Ala Gly Gln Pro Leu Leu Pro Ala Val Gly Ala  
20 25 30

Val Ile Thr Pro Gln Asn Gly Ala Gly Met Asp Lys Ala Ala Asn Gly  
 35 40 45

Val Pro Val Val Asn Ile Ala Thr Pro Asn Gly Ala Gly Ile Ser His  
 50 55 60

Asn Arg Phe Thr Asp Tyr Asn Val Gly Lys Glu Gly Leu Ile Leu Asn  
 65 70 75 80

Asn Ala Thr Gly Lys Leu Asn Pro Thr Gln Leu Gly Gly Leu Ile Gln  
 85 90 95

Asn Asn Pro Asn Leu Lys Ala Gly Gly Glu Ala Lys Gly Ile Ile Asn  
 100 105 110

Glu Val Thr Gly Gly Lys Arg Ser Leu Leu Gln Gly Tyr Thr Glu Val  
 115 120 125

Ala Gly Lys Ala Ala Asn Val Met Val Ala Asn Pro Tyr Gly Ile Thr  
 130 135 140

Cys Asp Gly Cys Gly Phe Ile Asn Thr Pro His Ala Thr Leu Thr Thr  
 145 150 155 160

Gly Lys Pro Val Met Asn Ala Asp Gly Ser Leu Gln Ala Leu Glu Val  
 165 170 175

Thr Glu Gly Ser Ile Thr Ile Asn Gly Ala Gly Leu Asp Gly Thr Arg  
 180 185 190

Ser Asp Ala Val Ser Ile Ile Ala Arg Ala Thr Glu Val Asn Ala Ala  
 195 200 205

Leu His Ala Lys Asp Leu Thr Val Thr Ala Gly Ala Asn Arg Val Thr  
 210 215 220

Ala Asp Gly Arg Val Arg Ala Leu Lys Gly Glu Gly Asp Val Pro Lys  
 225 230 235 240

Val Ala Val Asp Thr Gly Ala Leu Gly Gly Met Tyr Ala Arg Arg Ile  
 245 250 255

His Leu Thr Ser Thr Glu Ser Gly Val Gly Val Asn Leu Gly Asn Leu  
 260 265 270

Tyr Ala Arg Asp Gly Asp Ile Thr Leu Asp Ala Ser Gly Arg Leu Thr  
 275 280 285

Val Asn Asn Ser Leu Ala Thr Gly Ala Val Thr Ala Lys Gly Gln Gly  
 290 295 300

Val Thr Leu Thr Gly Asp His Lys Ala Gly Gly Asn Leu Ser Val Ser  
 305 310 315 320

Ser Arg Arg Asp Ile Val Leu Ser Asn Gly Thr Leu Asn Ser Asp Lys  
 325 330 335

Asp Leu Ser Leu Thr Ala Gly Gly Arg Ile Thr Gln Gln Asn Glu Lys  
 340 345 350

Leu Thr Ala Gly Arg Asp Val Thr Leu Ala Ala Lys Asn Ile Thr Gln  
 355 360 365

Asp Thr Ala Ser Gln Ile Asn Ala Ala Arg Asp Ile Val Thr Val Ala  
 370 375 380

Ser Asp Thr Leu Thr Thr Gln Gly Gln Ile Thr Ala Gly Gln Asn Leu  
 385 390 395 400

Thr Ala Ser Ala Thr Thr Leu Thr Gln Asp Gly Ile Leu Leu Ala Lys  
 405 410 415

Ser His Ala Gly Leu Asn Ala Gly Thr Leu Asn Asn Ser Gly Ala Val  
 420 425 430

Gln Gly Ala Thr Leu Thr Leu Gly Ser Thr Thr Leu Ser Asn Ser Gly  
 435 440 445

Ser Leu Leu Ser Gly Gly Pro Leu Thr Met Asn Thr Arg Asp Phe Thr  
 450 455 460

Gln Ser Gly Arg Thr Gly Ala Lys Gly Lys Val Asp Ile Met Ala Ser  
 465 470 475 480

Gly Lys Leu Thr Ser Thr Gly Leu Leu Val Thr Met His Leu Val Leu  
 485 490 495

Lys Ala Gln Asp Val Thr Gln Asn Gly Val Leu Ser Gly Gly Lys Gly  
 500 505 510

Leu Thr Val Ser Ala Thr Ser Ser Gly Lys Lys Ser Val Thr His Ser  
 515 520 525

Asp Ala Ala Met Thr Leu Asn Val Thr Thr Val Ala Leu Asp Gly Glu  
 530 535 540

Thr Ser Ala Gly Asp Thr Leu Arg Val Gln Ala Asp Lys Leu Ser Thr  
 545 550 555 560

Ala Ala Gly Ala Gln Leu Gln Ser Gly Lys Asn Leu Ser Ile Asn Ala  
 565 570 575

Arg Asp Ala Arg Leu Ala Gly Thr Gln Ala Ala Gln Gln Thr Met Val  
 580 585 590

Val Asn Ala Ser Glu Lys Leu Thr His Ser Gly Lys Ser Ser Ala Pro  
 595 600 605

Ser Leu Ser Leu Ser Ala Pro Glu Leu Thr Ser Ser Gly Val Leu Val  
 610 615 620

Gly Ser Ala Leu Asn Thr Gln Ser Gln Thr Leu Thr Asn Ser Gly Leu  
 625 630 635 640

Leu Gln Gly Glu Ala Ser Leu Thr Val Asn Thr Gln Arg Leu Asp Asn  
 645 650 655

Gln Gln Asn Gly Thr Leu Tyr Ser Ala Ala Asp Leu Thr Leu Asp Ile  
 660 665 670

Pro Asp Ile Arg Asn Ser Gly Leu Ile Thr Gly Asp Asn Gly Leu Met  
 675 680 685

Leu Asn Ala Val Ser Leu Ser Asn Pro Gly Lys Ile Ile Ala Asp Thr  
 690 695 700

Leu Ser Val Arg Ala Thr Thr Leu Asp Gly Asp Gly Leu Leu Gln Gly  
 705 710 715 720

Ala Gly Ala Leu Ala Leu Ala Gly Asp Thr Leu Ser Gln Gly Ser His  
 725 730 735

Gly Arg Trp Leu Thr Ala Asp Asp Leu Ser Leu Arg Gly Lys Thr Leu  
 740 745 750

Asn Thr Ala Gly Thr Thr Gln Gly Gln Asn Ile Thr Val Gln Ala Asp  
 755 760 765

Arg Trp Ala Asn Ser Gly Ser Val Leu Ala Thr Gly Asn Leu Thr Ala  
 770 775 780

Ser Ala Thr Gly Gln Leu Thr Ser Thr Gly Asp Ile Met Ser Gln Gly  
 785 790 795 800

Asp Thr Thr Leu Lys Ala Ala Thr Thr Asp Asn Arg Gly Ser Leu Leu  
 805 810 815

Ser Ala Gly Thr Leu Ser Leu Asp Gly Asn Ser Leu Asp Asn Arg Gly  
 820 825 830

Thr Val Gln Gly Asn His Val Thr Ile Arg Gln Asn Ser Val Thr Asn  
 835 840 845

Ser Gly Thr Leu Thr Gly Ile Ala Ala Leu Thr Leu Ala Ala Arg Met  
 850 855 860

Ala Ser Pro Gln Pro Ala Leu Met Asn Asn Gly Gly Ser Leu Leu Thr  
 865 870 875 880

Ser Gly Asp Leu Thr Ile Thr Ala Gly Ser Ile Thr Ser Ser Gly His  
 885 890 895

Trp Gln Gly Lys Arg Val Leu Ile Thr Ala Asp Ser Leu Ala Asn Ser  
 900 905 910

Gly Ala Ile Gln Ala Ala Asp Ser Leu Thr Ala Arg Leu Thr Gly Glu  
 915 920 925

Leu Val Ser Thr Ala Gly Ser Lys Val Thr Ser Asn Gly Glu Met Ala  
 930 935 940

Leu Ser Ala Leu Asn Leu Ser Asn Ser Gly Gln Trp Ile Ala Lys Asn  
 945 950 955 960

Leu Thr Leu Lys Ala Asn Ser Leu Thr Ser Ala Gly Asp Ile Thr Gly  
 965 970 975

Val Asp Thr Leu Thr Leu Thr Val Asn Gln Thr Leu Asn Asn Gln Ala  
 980 985 990

Asn Gly Lys Leu Leu Ser Ala Gly Val Leu Thr Leu Lys Ala Asp Ser  
 995 1000 1005

Val Thr Asn Asp Gly Gln Leu Gln Gly Asn Val Thr Thr Ile Thr  
 1010 1015 1020

Ala Gly Gln Leu Thr Asn Gly Gly His Leu Gln Gly Glu Thr Leu  
 1025 1030 1035

Thr Leu Thr Ala Ser Gly Gly Val Asn Asn Arg Ser Gly Gly Val  
 1040 1045 1050

Leu Met Ser Arg Asn Ala Leu Asn Val Ser Thr Ala Thr Leu Ser  
 1055 1060 1065

Asn Gln Ser Thr Ile Gln Gly Gly Gly Gly Val Ser Leu Asn Ala  
 1070 1075 1080

Thr Asp 1085	Arg Leu Gln Asn Asp 1090	Gly Lys Ile Leu Ser 1095	Gly Ser Asn
Leu Thr 1100	Leu Thr Ala Gln Val 1105	Leu Ala Asn Thr 1110	Gly Ser Gly Leu
Val Gln 1115	Ala Ala Thr Leu Leu 1120	Leu Asp Val Val 1125	Asn Thr Val Asn
Gly Gly 1130	Arg Val Leu Ala Thr 1135	Gly Ser Asp Val 1140	Lys Gly Thr Thr
Leu Asn 1145	Asn Thr Gly Thr Leu 1150	Gln Gly Ala Thr 1155	Leu Val Asn Tyr
His Thr 1160	Phe Ser Ser Gly Thr 1165	Leu Leu Gly Thr 1170	Ser Gly Leu Gly
Val Lys 1175	Gly Ser Ser Leu Leu 1180	Gln Asn Gly Thr 1185	Gly Arg Leu Tyr
Ser Ala 1190	Gly Asn Leu Leu Leu 1195	Asp Ala Gln Asp 1200	Phe Ser Gly Gln
Gly Gln 1205	Val Val Ala Thr Gly 1210	Asp Val Thr Leu 1215	Lys Leu Ile Ala
Ala Leu 1220	Thr Asn His Gly Thr 1225	Leu Ala Ala Gly 1230	Lys Thr Leu Ser
Val Thr 1235	Ser Gln Asn Ala Ile 1240	Thr Asn Gly Gly 1245	Val Met Gln Gly
Asp Ala 1250	Met Val Leu Gly Ala 1255	Gly Glu Ala Phe 1260	Thr Asn Asn Gly
Leu Thr 1265	Ala Gly Lys Gly Asn 1270	Ser Val Phe Ser 1275	Ala Gln Arg Leu
Phe Leu 1280	Asn Ala Pro Gly Ser 1285	Leu Gln Gly Gly 1290	Gly Asp Val Ser
Leu Asn 1295	Ser Arg Ser Asp Ile 1300	Thr Ile Ser Gly 1305	Phe Thr Gly Thr
Ala Gly 1310	Ser Leu Thr Met Asn 1315	Val Ala Gly Thr 1320	Leu Leu Asn Ser

Ala	Leu	Ile	Tyr	Ala	Gly	Asn	Asn	Leu	Lys	Leu	Phe	Thr	Asp	Arg
1325						1330					1335			
Leu	His	Asn	Gln	His	Gly	Asp	Ile	Leu	Ala	Gly	Asn	Ser	Leu	Trp
1340						1345					1350			
Val	Gln	Lys	Asp	Ala	Ser	Gly	Gly	Ala	Asn	Thr	Glu	Ile	Ile	Asn
1355						1360					1365			
Asn	Ser	Gly	Asn	Ile	Glu	Thr	His	Gln	Gly	Asp	Ile	Val	Val	Arg
1370						1375					1380			
Thr	Gly	His	Leu	Leu	Asn	Gln	Arg	Glu	Gly	Phe	Ser	Ala	Thr	Thr
1385						1390					1395			
Thr	Thr	Arg	Thr	Asn	Pro	Ser	Ser	Ile	Gln	Gly	Met	Gly	Asn	Ala
1400						1405					1410			
Leu	Val	Asp	Ile	Pro	Leu	Ser	Leu	Leu	Pro	Asp	Gly	Ser	Tyr	Gly
1415						1420					1425			
Tyr	Phe	Thr	Arg	Glu	Val	Glu	Asn	Gln	His	Gly	Thr	Pro	Cys	Asn
1430						1435					1440			
Gly	His	Gly	Ala	Cys	Asn	Ile	Thr	Met	Asp	Thr	Leu	Tyr	Tyr	Tyr
1445						1450					1455			
Ala	Pro	Phe	Ala	Asp	Ser	Ala	Thr	Gln	Arg	Phe	Leu	Ser	Ser	Gln
1460						1465					1470			
Asn	Ile	Thr	Thr	Val	Thr	Gly	Ala	Asp	Asn	Pro	Ala	Gly	Arg	Ile
1475						1480					1485			
Ala	Ser	Gly	Arg	Asn	Leu	Ser	Ala	Glu	Ala	Glu	Arg	Leu	Glu	Asn
1490						1495					1500			
Arg	Ala	Ser	Phe	Ile	Leu	Ala	Asn	Gly	Asp	Ile	Ala	Leu	Ser	Gly
1505						1510					1515			
Arg	Glu	Leu	Ser	Asn	Gln	Ser	Trp	Gln	Thr	Gly	Thr	Glu	Asn	Glu
1520						1525					1530			
Tyr	Leu	Val	Tyr	Arg	Tyr	Asp	Pro	Lys	Thr	Phe	Tyr	Gly	Ser	Tyr
1535						1540					1545			
Ala	Thr	Gly	Ser	Leu	Asp	Lys	Leu	Pro	Leu	Leu	Ser	Pro	Glu	Phe
1550						1555					1560			
Glu	Asn	Asn	Thr	Ile	Arg	Phe	Ser	Leu	Asp	Gly	Arg	Glu	Lys	Asp
1565						1570					1575			

Tyr	Thr	Pro	Gly	Lys	Thr	Tyr	Tyr	Ser	Val	Ile	Gln	Ala	Gly	Gly
1580						1585					1590			
Asp	Val	Lys	Thr	Arg	Phe	Thr	Ser	Ser	Ile	Asn	Asn	Gly	Thr	Thr
1595						1600					1605			
Thr	Ala	His	Ala	Gly	Ser	Val	Ser	Pro	Val	Val	Ser	Ala	Pro	Val
1610						1615					1620			
Leu	Asn	Thr	Leu	Ser	Gln	Gln	Thr	Gly	Gly	Asp	Ser	Leu	Thr	Gln
1625						1630					1635			
Thr	Ala	Leu	Gln	Gln	Tyr	Glu	Pro	Val	Val	Val	Gly	Ser	Pro	Gln
1640						1645					1650			
Trp	His	Asp	Glu	Leu	Ala	Gly	Ala	Leu	Lys	Asn	Ile	Ala	Gly	Gly
1655						1660					1665			
Ser	Pro	Leu	Thr	Gly	Gln	Thr	Gly	Ile	Ser	Asp	Asp	Trp	Pro	Leu
1670						1675					1680			
Pro	Ser	Gly	Asn	Asn	Gly	Tyr	Leu	Val	Pro	Ser	Thr	Asp	Pro	Asp
1685						1690					1695			
Ser	Pro	Tyr	Leu	Ile	Thr	Val	Asn	Pro	Lys	Leu	Asp	Gly	Leu	Gly
1700						1705					1710			
Gln	Val	Asp	Ser	His	Leu	Phe	Ala	Gly	Leu	Tyr	Glu	Leu	Leu	Gly
1715						1720					1725			
Ala	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Glu	Thr	Ala	Pro	Ser	Tyr	Thr
1730						1735					1740			
Asp	Glu	Lys	Gln	Phe	Leu	Gly	Ser	Ser	Tyr	Phe	Leu	Asp	Arg	Leu
1745						1750					1755			
Gly	Leu	Lys	Pro	Glu	Lys	Asp	Tyr	Arg	Phe	Leu	Gly	Asp	Ala	Val
1760						1765					1770			
Phe	Asp	Thr	Arg	Tyr	Val	Ser	Asn	Ala	Val	Leu	Ser	Arg	Thr	Gly
1775						1780					1785			
Ser	Arg	Tyr	Leu	Asn	Gly	Leu	Gly	Ser	Asp	Thr	Glu	Gln	Met	Arg
1790						1795					1800			
Tyr	Leu	Met	Asp	Asn	Ala	Ala	Arg	Gln	Gln	Lys	Gly	Leu	Gly	Leu
1805						1810					1815			



Glu Phe Gly Val Ala Leu Thr Ala Glu Gln Ile Ala Gln Leu Asp  
 1820 1825 1830

Gly Ser Ile Leu Trp Trp Glu Ser Val Thr Ile Asn Gly Gln Thr  
 1835 1840 1845

Val Met Val Pro Lys Leu Tyr Leu Ser Pro Glu Asp Ile Thr Leu  
 1850 1855 1860

His Asn Gly Ser Val Ile Ser Gly Asn Asn Val Gln Leu Ala Gly  
 1865 1870 1875

Gly Asn Ile Thr Asn Ser Gly Gly Ser Ile Asn Ala Gln Asn Asp  
 1880 1885 1890

Leu Ser Leu Asp Ser Ser Gly Tyr Ile Asp Asn Leu Asn Ala Gly  
 1895 1900 1905

Leu Ile Ser Ala Gly Gly Ser Leu Asp Leu Ser Ala Ile Gly Asp  
 1910 1915 1920

Ile Ser Asn Ile Ser Ser Val Ile Ser Gly Lys Thr Val Gln Leu  
 1925 1930 1935

Glu Ser Val Ser Gly Asn Ile Ser Asn Ile Thr Arg Arg Gln Gln  
 1940 1945 1950

Trp Asn Ala Gly Ser Asp Ser Gln Tyr Gly Gly Val His Leu Ser  
 1955 1960 1965

Gly Thr Asp Thr Gly Pro Val Ala Thr Ile Lys Gly Thr Asp Ser  
 1970 1975 1980

Leu Ser Leu Asp Ala Gly Lys Asn Ile Asp Ile Thr Gly Ala Thr  
 1985 1990 1995

Val Ser Ser Gly Gly Asp Leu Gly Met Ser Ala Gly Asn Asp Ile  
 2000 2005 2010

Asn Ile Ala Ala Asn Leu Ile Ser Gly Ser Lys Ser Gln Ser Gly  
 2015 2020 2025

Phe Trp His Thr Asp Asp Asn Ser Ser Ser Ser Thr Thr Ser Gln  
 2030 2035 2040

Gly Ser Ser Ile Ser Ala Gly Gly Asn Leu Ala Met Ala Ala Gly  
 2045 2050 2055

His Asn Leu Asp Val Thr Ala Ser Ser Val Ser Ala Gly His Ser  
 2060 2065 2070

Ala Leu 2075	Leu Ser Cys Arg Ser 2080	Arg Pro Ser Leu Glu 2085	Cys Ser Gln
Gly Lys 2090	Ala Lys Thr Ser Arg 2095	Asn Gly Arg Ser Glu 2100	Ser His Glu
Ser His 2105	Ala Ala Val Ser Thr 2110	Val Thr Ala Gly Asp 2115	Asn Phe Leu
Leu Val 2120	Ala Gly Arg Asp Ile 2125	Ala Ser Gln Ala Ala 2130	Gly Met Ala
Ala Glu 2135	Asn Asn Val Val Ile 2140	Arg Gly Gly Arg Asp 2145	Val Asn Leu
Val Ala 2150	Glu Ser Ala Gly Ala 2155	Gly Asp Ser Tyr Thr 2160	Ser Lys Lys
Lys Lys 2165	Glu Ile Asn Glu Thr 2170	Val Arg Gln Gln Gly 2175	Thr Glu Ile
Ala Ser 2180	Gly Gly Asp Thr Thr 2185	Val Asn Ala Gly Arg 2190	Asp Ile Thr
Ala Val 2195	Ala Ser Ser Val Thr 2200	Ala Thr Gly Asn Ile 2205	Ser Val Asn
Ala Gly 2210	Arg Asp Val Ala Leu 2215	Thr Thr Ala Thr Glu 2220	Ser Asp Tyr
His Tyr 2225	Leu Glu Thr Lys Lys 2230	Lys Ser Gly Gly Phe 2235	Leu Ser Lys
Lys Thr 2240	Thr Arg Thr Ile Ser 2245	Glu Asp Ser Ala Thr 2250	Arg Glu Ala
Gly Ser 2255	Leu Leu Ser Gly Asn 2260	Arg Val Thr Val Asn 2265	Ala Gly Asp
Asn Leu 2270	Thr Val Glu Gly Ser 2275	Asp Val Val Ala Asp 2280	Arg Asp Val
Ser Leu 2285	Ala Ala Gly Asn His 2290	Val Asp Val Leu Ala 2295	Ala Thr Ser
Thr Asp 2300	Thr Ser Trp Arg Phe 2305	Lys Glu Thr Lys Lys 2310	Ser Gly Leu

Met Gly Thr Gly Gly Ile Gly Phe Thr Ile Gly Ser Ser Lys Thr  
 2315 2320 2325  
 Thr His Asp Arg Arg Glu Ala Gly Thr Thr Gln Ser Gln Ser Ala  
 2330 2335 2340  
 Ser Thr Ile Gly Ser Thr Ala Gly Asn Val Ser Ile Thr Ala Gly  
 2345 2350 2355  
 Lys Gln Ala His Ile Ser Gly Ser Asp Val Ile Ala Asn Arg Asp  
 2360 2365 2370  
 Ile Ser Ile Thr Gly Asp Ser Val Val Val Asp Pro Gly His Asp  
 2375 2380 2385  
 Arg Arg Thr Val Asp Glu Lys Phe Glu Gln Lys Lys Ser Gly Leu  
 2390 2395 2400  
 Thr Val Ala Leu Ser Gly Thr Val Gly Ser Ala Ile Asn Asn Ala  
 2405 2410 2415  
 Val Thr Ser Ala Gln Glu Thr Lys Glu Ser Ser Asp Ser Arg Leu  
 2420 2425 2430  
 Lys Ala Leu Gln Ala Thr Lys Thr Ala Leu Ser Gly Val Gln Ala  
 2435 2440 2445  
 Gly Gln Ala Ala Thr Met Ala Ser Ala Thr Gly Asp Pro Asn Ala  
 2450 2455 2460  
 Gly Val Ser Leu Ser Leu Thr Thr Gln Lys Ser Lys Ser Gln Gln  
 2465 2470 2475  
 His Ser Glu Ser Asp Thr Val Ser Gly Ser Thr Leu Asn Ala Gly  
 2480 2485 2490  
 Asn Asn Leu Ser Val Val Ala Thr Gly Lys Asn Arg Gly Asp Asn  
 2495 2500 2505  
 Arg Gly Asp Ile Val Ile Ala Gly Ser Gln Leu Lys Ala Gly Gly  
 2510 2515 2520  
 Asn Thr Ser Leu Asp Ala Ala Asn Asp Ile Leu Leu Ser Gly Ala  
 2525 2530 2535  
 Ala Asn Thr Gln Lys Thr Thr Gly Arg Asn Ser Ser Ser Gly Gly  
 2540 2545 2550  
 Gly Val Gly Val Ser Ile Gly Ala Gly Lys Gly Ala Gly Ile Ser  
 2555 2560 2565

Ala Phe Ala Ser Val Asn Ala Ala Lys Gly Arg Glu Lys Gly Asn  
 2570 2575 2580  
 Gly Thr Thr Thr Asp Lys Thr Val Thr Ile Asn Ser Gly Arg Asp  
 2585 2590 2595  
 Thr Val Leu Asn Gly Ala Gln Val Asn Gly Asn Arg Ile Ile Ala  
 2600 2605 2610  
 Asp Val Gly His Asp Leu Leu Ile Ser Ser Gln Gln Asp Thr Ser  
 2615 2620 2625  
 Lys Tyr Asp Ser Lys Gln Thr Ser Val Ala Ala Gly Gly Ser Phe  
 2630 2635 2640  
 Thr Phe Gly Ser Met Thr Gly Ser Gly Tyr Ile Ala Ala Ser Arg  
 2645 2650 2655  
 Asp Lys Met Lys Ser Arg Phe Asp Ser Val Ala Glu Gln Thr Gly  
 2660 2665 2670  
 Met Phe Ala Arg Val Met Val Ala Ser Thr Ser Gln Trp Val Asn  
 2675 2680 2685  
 Ile Pro Asn Trp Met Val Arg Ser Leu Pro His Cys His Thr Gly  
 2690 2695 2700  
 Glu Lys Pro Pro Gly Tyr Arg Thr Leu Gly Leu Val Thr Leu Gln  
 2705 2710 2715  
 Arg Ser Gly Ile Ile Lys Ser Ser His Arg Trp Asn Gln Ser  
 2720 2725 2730  
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 Met Met Leu Lys Lys Thr Ile Phe Ile Leu Thr Leu Phe Ser Gly Asn  
 1 5 10 15  
 Val Ile Ala Ala Thr Val Glu Leu Gly Phe Glu Asn Glu Gln Tyr Asn  
 20 25 30  
 Tyr Ala Tyr Arg Ser Ala Asp Val Phe Met Pro Tyr Ile Lys Ser Asn  
 35 40 45  
 Phe Asn Pro Val Thr Asp Ser Ala Leu Asn Val Ser Leu Thr Tyr Met  
 50 55 60  
 Tyr Gln Asp Gln Tyr Gly Lys Lys His Lys Lys Thr Ser Glu Asp Arg  
 65 70 75 80

Phe Lys Thr Asn Arg Asp Arg Ile Glu Leu Tyr Leu Lys Gly Tyr Thr  
                             85                            90                            95

Leu Asn Arg Gly Ala Tyr Ser Phe Ser Pro Ser Ala Gly Phe Arg Tyr  
                             100                            105                            110

Glu Ser Trp Asp Val Asn Tyr Asp Asn Pro Lys Lys Gln Asp Lys Trp  
                             115                            120                            125

Lys Leu Glu Leu Arg Phe Tyr Pro Asn Met Thr Tyr Lys Leu Asn Asp  
                             130                            135                            140

Gln Leu Ser Leu Tyr Met Asn Gly Phe Val Ala Pro Val Phe Phe Lys  
                             145                            150                            155                            160

Thr Gln Gln Glu Ser Arg Lys Asp Asn Asn Tyr Val Lys Gly Lys Leu  
                             165                            170

Gly Ala Lys Arg Tyr Asn Asn Asp Tyr Tyr Gln Glu Leu Gln Ile Leu  
                             180                            185

Gly Val Arg Tyr Lys Phe Asn Asn Asp Asn Thr Leu Trp Ala Ser Val  
                             195                            200                            205

Tyr Asn Glu Arg Lys Tyr Asn Gln His Ser Ser Lys Tyr Asp Arg Trp  
                             210                            215                            220

Gln Leu Arg Gly Gly Tyr Asp Phe Lys Val Thr Glu Glu Phe Val Leu  
                             225                            230                            235                            240

Ser Pro Phe Ile Arg Tyr Asp Leu Ser Tyr Arg Glu Lys Asn Leu Glu  
                             245                            250                            255

Ser Thr Ser Asn Asn Gly Leu Ser Lys Asn Asn Lys Glu Ile Arg Thr  
                             260                            265                            270

Gly Ala Ser Phe Ser Tyr Lys Ile Ile Pro Ser Val Lys Leu Val Gly  
                             275                            280                            285

Glu Ile Tyr Arg Gln Thr Thr Asn Ile Glu Asn Tyr Tyr Gly Glu His  
                             290                            295                            300

Ser Glu Asp Lys Asn Arg Met Phe Tyr Lys Leu Gly Ile Asn Lys Thr  
                             305                            310                            315                            320

Phe

<210> 45 <211> 587 <212> PRT <213> Escherichia coli <400> 45

Met Gln His Arg Gln Lys Asn Ile Leu Thr Lys Thr Ser Leu Leu Ser  
1 5 10 15

Arg Ala Leu Ser Val Pro Cys Cys Asp Met Phe Arg Arg Gly Ser Pro  
20 25 30

Trp Ile Cys Tyr Leu Ser Leu Ser Val Phe Ser Gly Cys Phe Ile Pro  
35 40 45

Ala Phe Ser Ser Pro Ala Ala Met Leu Ser Pro Gly Asp Arg Ser Ala  
50 55 60

Ile Gln Gln Gln Gln Gln Gln Leu Leu Asp Glu Asn Gln Arg Gln Arg  
65 70 75 80

Asp Ala Leu Glu Arg Pro Leu Thr Ile Thr Pro Ser Pro Glu Thr Ser  
85 90 95

Ala Gly Thr Glu Gly Pro Cys Phe Thr Val Ser Ser Ile Val Val Ser  
100 105 110

Gly Ala Thr Arg Leu Thr Ser Ala Glu Thr Asp Arg Leu Val Pro Trp  
115 120 125

Val Asn Gln Cys Leu Asn Ile Thr Gly Leu Thr Ala Val Thr Asp Ala  
130 135 140

Val Thr Asp Gly Tyr Ile Arg Arg Gly Tyr Ile Thr Ser Arg Ala Phe  
145 150 155 160

Leu Thr Glu Gln Asp Leu Ser Gly Gly Val Leu His Ile Thr Val Met  
165 170 175

Glu Gly Arg Leu Gln Gln Ile Arg Ala Glu Gly Ala Asp Leu Pro Ala  
180 185 190

Arg Thr Leu Lys Met Val Phe Pro Gly Met Glu Gly Lys Val Leu Asn  
195 200 205

Leu Arg Asp Ile Glu Gln Gly Met Glu Gln Ile Asn Arg Leu Arg Thr  
210 215 220

Glu Pro Val Gln Ile Glu Ile Ser Pro Gly Asp Arg Glu Gly Trp Ser  
225 230 235 240

Val Val Thr Leu Thr Ala Leu Pro Glu Trp Pro Val Thr Gly Ser Val  
245 250 255

Gly Ile Asp Asn Ser Gly Gln Lys Ser Thr Gly Thr Gly Gln Leu Asn  
 260 265 270

Gly Val Leu Ser Phe Asn Asn Pro Leu Gly Leu Ala Asp Asn Trp Phe  
 275 280 285

Val Ser Gly Gly Arg Ser Ser Asp Phe Ser Val Ser His Asp Ala Arg  
 290 295 300

Asn Phe Ala Ala Gly Val Ser Leu Pro Tyr Gly Tyr Thr Leu Val Asp  
 305 310 315 320

Tyr Thr Tyr Ser Trp Ser Asp Tyr Leu Ser Thr Ile Asp Asn Arg Gly  
 325 330 335

Trp Arg Trp Arg Ser Thr Gly Asp Leu Gln Thr His Arg Leu Gly Leu  
 340 345 350

Ser His Val Leu Phe Arg Asn Gly Asp Met Lys Thr Ala Leu Thr Gly  
 355 360 365

Gly Leu Gln His Arg Ile Ile His Asn Tyr Leu Asp Asp Val Leu Leu  
 370 375 380

Gln Gly Ser Ser Arg Lys Leu Thr Ser Phe Ser Val Gly Leu Asn His  
 385 390 395 400

Thr His Lys Phe Leu Gly Gly Val Gly Thr Leu Asn Pro Val Phe Thr  
 405 410 415

Arg Gly Met Pro Trp Phe Gly Ala Glu Ser Asp His Gly Lys Arg Gly  
 420 425 430

Asp Leu Pro Val Asn Gln Phe Arg Lys Trp Ser Val Ser Ala Ser Phe  
 435 440 445

Gln Arg Pro Val Thr Asp Arg Val Trp Trp Leu Thr Ser Ala Tyr Ala  
 450 455 460

Gln Trp Ser Pro Asp Arg Leu His Gly Val Glu Gln Leu Ser Leu Gly  
 465 470 475 480

Gly Glu Ser Ser Val Arg Gly Phe Lys Asp Gln Tyr Ile Ser Gly Asn  
 485 490 495

Asn Gly Gly Tyr Leu Arg Asn Glu Leu Ser Trp Ser Leu Phe Ser Leu  
 500 505 510

Pro Tyr Val Gly Thr Val Arg Ala Val Ala Ala Leu Asp Gly Gly Trp  
 515 520 525

Leu His Ser Asp Ser Asp Asp Pro Tyr Ser Ser Gly Thr Leu Trp Gly  
530 535 540

Ala Ala Ala Gly Leu Ser Thr Thr Ser Gly His Val Ser Gly Ser Phe  
545 550 555 560

Thr Ala Gly Leu Pro Leu Val Tyr Pro Asp Trp Leu Ala Pro Asp His  
565 570 575

Leu Thr Val Tyr Trp Arg Val Ala Val Ala Phe  
580 585

<210> 46 <211> 744 <212> PRT <213> Escherichia coli <400> 46

Met Asn Lys His Thr Leu Leu Leu Thr Val Leu Phe Leu Asn Leu Ile  
1 5 10 15

Cys Thr Pro Val Phe Ala Gln Asn Trp Gln Val Ala Thr Phe Gly Gln  
20 25 30

Ser Thr Asp Leu Asn Phe Ser Ser Leu Ile Asp Ser Ala Lys Ile Gly  
35 40 45

Arg Asn Asn Ala Trp Leu Ala Gly Asn Asn Asn Phe Leu Glu Ala Gly  
50 55 60

Lys Phe Tyr Thr Leu Pro Thr Asp Phe Phe Ile Glu Ser Arg Gly Gly  
65 70 75 80

Lys Ile Ala Asn Ser His Asp Gly Met Thr Val Phe Tyr Thr Ile Val  
85 90 95

Pro Val Thr Gln Thr Phe Arg Leu Glu Ala Asp Leu Thr Leu Glu Gln  
100 105 110

Ile Gly Pro Glu Val Asn Gly Lys Ser Pro Ala Gly Gln Glu Gly Ala  
115 120 125

Gly Leu Phe Val Arg Asp Ile Ile Gly Pro Gln Arg Gln Glu Pro Gln  
130 135 140

Ser Ala Gly Thr Glu Glu Tyr Pro Gln Ala Ser Asn Ile Leu Met Asn  
145 150 155 160

Ala Phe Ile Thr Gln Asn Lys Lys Asn Asp Asn Leu Val Gln Ile Thr  
165 170 175

Ser Ile Val Arg Glu Gly Val Ile Lys Thr Trp Gly Asn Glu Gly Ile  
180 185 190



Thr Ile Lys Lys Gln Pro Ile Ile Glu Asn Ile Asn Phe Thr Gln Lys  
 195 200 205

Arg Asn Ile His Met Thr Ile Glu Arg Leu Pro Glu Lys Phe Ile Leu  
 210 215 220

Thr Ala Phe Asp Thr Asp Arg Lys Glu Asn Gln Ser Trp Gln Phe Ser  
 225 230 235 240

Asp Tyr Ser Gly Phe Met Asn Gln Leu Asp Asn Asn Ser Leu Ala Ile  
 245 250 255

Gly Phe Phe Ala Ala Arg Asn Ala Lys Leu Arg Val Lys Asn Ala Ser  
 260 265 270

Phe Lys Pro Gly Lys Pro Leu Val Asp Tyr Lys Gln Leu Thr Ser Arg  
 275 280 285

Gln Phe Ser Arg Val Arg His Lys Ala Pro Glu Leu Phe Leu Ala Ser  
 290 295 300

Pro Gln Ser Val Val Arg Asn Ser Thr Thr Leu Gln Phe Leu Ala Asn  
 305 310 315 320

Gln Ala Gly Ile Val Ser Ile Asp Asn Asp Lys Gln Thr Lys Gln Val  
 325 330 335

Gln Ala Gly Glu Leu Val Gln Phe Pro Val Thr Leu Gln Lys Lys His  
 340 345 350

Asn Asp Phe Thr Val Asn Phe Asn Val Asp Gly Asn Ile Ser Lys Lys  
 355 360 365

Ala Ile Arg Ile Glu Gln Val Lys Ser Asn Leu Thr Asp Pro Tyr Glu  
 370 375 380

Ile Tyr Val Cys Ser Asp Cys Arg Gln Gly Ala Arg Gly Ser Lys Asn  
 385 390 395 400

Asp Pro Val Asp Leu Gln Thr Ala Val Lys Phe Val Ala Pro Gly Gly  
 405 410 415

Asn Ile Tyr Leu Asn Asp Gly Gln Tyr His Gly Ile Thr Leu Asp Arg  
 420 425 430

Glu Leu Ser Gly Ile Pro Gly Lys Tyr Lys Thr Ile Ser Ala Ile Asn  
 435 440 445

Pro His Lys Ala Ile Phe Ile Asn Lys Thr Phe Asn Leu Asp Ala Ser  
 450 455 460  
 Tyr Trp His Leu Lys Ser Val Val Phe Asp Gly Asn Val Asp Asn Gly  
 465 470 475 480  
 Asn Asn Lys Pro Ala Tyr Leu Arg Ile Ala Gly Ser Tyr Asn Ile Ile  
 485 490 495  
 Glu His Val Ile Ala Arg Asn Asn Asp Asp Thr Gly Ile Ser Ile Ser  
 500 505 510  
 Ala Lys Asp Lys Asn Arg Phe Phe Trp Pro Ala His Asn Leu Val Leu  
 515 520 525  
 Asn Ser Asp Ser Tyr Asn Asn Leu Asp Leu Ser Gly Ile Asn Ala Asp  
 530 535 540  
 Gly Phe Ala Ala Lys Leu Gly Val Gly Pro Gly Asn Ile Phe Arg Gly  
 545 550 555 560  
 Cys Ile Ala His Asn Asn Ala Asp Asp Gly Trp Asp Leu Phe Asn Lys  
 565 570 575  
 Ile Glu Asp Gly Pro Asn Ala Ser Val Thr Ile Glu Asn Ser Val Ala  
 580 585 590  
 Tyr Glu Asn Gly Leu Pro Tyr Asn Lys Ala Asp Ile Leu Lys Gly Ser  
 595 600 605  
 Ile Gly Asn Gly Gly Glu Gly Gln Pro Ser Lys Ser Gln Val Ile Asn  
 610 615 620  
 Ser Ile Ala Ile Asn Asn Asn Met Asp Gly Phe Thr Asp Asn Phe Asn  
 625 630 635 640  
 Thr Gly Ser Leu Ile Val Arg Asn Asn Ile Ala Met Asn Asn Ala Arg  
 645 650 655  
 Tyr Asn Tyr Ile Leu Arg Thr Asn Pro Tyr Lys Phe Pro Ser Ser Ile  
 660 665 670  
 Leu Phe Asp Asn Asn Tyr Ser Ile Arg Asp Asp Trp Glu Asn Lys Ile  
 675 680 685  
 Lys Asp Phe Leu Gly Asp Thr Val Asn Ser Val Asn Tyr Lys Leu Leu  
 690 695 700  
 Val Ser His Glu Thr Gly Pro Val Gln Lys Asp Leu Phe Phe Thr Arg  
 705 710 715 720

Asp Asp Ser Gly Asn Ile Ile Tyr Pro Asp Phe Phe Leu Asn Ile Ile  
                   725                  730                  735

Asn Lys Phe Asn Glx Thr Met Pro  
                   740

<210> 47 <211> 136 <212> PRT <213> Escherichia coli <400> 47

Met Lys Thr Phe Ile Lys Thr Leu Leu Val Ala Val Thr Ile Leu Phe  
   1                  5                  10                  15

Ser Val Phe Ala Thr Ala Lys Gln Val Lys Leu Pro Asn Asn Ile Lys  
                   20                  25                  30

Tyr Val Asn Thr Thr Glu Ala Phe Ser Cys Thr Glu Ile Asp Gly Met  
           35                  40                  45

Asn Cys Gln Thr Lys Asn Pro Phe Asn Tyr Lys Asp Asn Ser Tyr Val  
       50                  55                  60

Phe Val Leu Glu Arg Gly Gly Ala Trp Cys Tyr Asp Tyr Thr Val Ser  
   65                  70                  75                  80

Val Leu Asn Leu Lys Thr Gly Lys Ala Gln Met Leu Glu Tyr Lys Asp  
                   85                  90                  95

Asn Gln Leu Cys Ser Gly Ser Asn Lys Pro Phe Phe Glu Ile Lys Asn  
                   100                  105                  110

Gly Val Pro Thr Val Gly Val Ile Asp Thr Ser Gly Lys Pro Val Val  
           115                  120                  125

Val Ala Leu Asp Lys Leu Lys Thr  
       130                  135

<210> 48 <211> 225 <212> PRT <213> Escherichia coli <400> 48

Met Gln Leu Pro Val Lys Leu Leu Met Ser Leu Ile Ser Leu Val Ser  
   1                  5                  10                  15

Val Ile Ala Arg Ala Gly Lys Tyr Lys Asn Tyr Ile Arg Asp Glu Ile  
           20                  25                  30

Lys Tyr Trp Arg Tyr Thr Ser Tyr Lys Gly Gly Glu Phe Pro Glu Gly  
       35                  40                  45

Phe Thr Asp Glu Lys Phe Ser Ser Ala Ile Tyr Asn Gly Arg Ile Phe  
       50                  55                  60

Thr Met Lys Arg Leu His Thr Leu Met Leu Phe Leu Ala Val Leu Phe  
65 70 75 80

Thr Gly Phe Asn Val Glu Ala Ala Ser Val Lys Gln Ala Leu Ser Cys  
85 90 95

Asp Pro Asn Ala Arg Ala Glu Gln Pro Gly Ala Cys Pro Thr Thr Tyr  
100 105 110

Glu Leu Tyr Glu Gly Asp Ala Ala Tyr Lys Ala Ala Leu Asp Lys Ala  
115 120 125

Leu Lys Pro Val Gly Leu Ser Gly Met Phe Gly Lys Gly Gly Tyr Met  
130 135 140

Asp Gly Pro Gly Gly Asn Val Thr Pro Val Thr Ile Asn Gly Thr Val  
145 150 155 160

Trp Leu Gln Gly Asp Gly Cys Lys Ala Asn Thr Cys Gly Trp Asp Phe  
165 170 175

Ile Val Thr Leu Tyr Asn Pro Lys Thr His Glu Val Val Gly Tyr Arg  
180 185 190

Tyr Phe Gly Leu Asp Asp Pro Ala Tyr Leu Val Trp Phe Gly Glu Ile  
195 200 205

Gly Val His Glu Phe Ala Tyr Leu Val Lys Asn Tyr Val Ala Ala Val  
210 215 220

Asn  
225

<210> 49 <211> 721 <212> PRT <213> Escherichia coli <400> 49

Met Lys Thr Gln Ile Thr Phe Ala Ala Leu Leu Pro Ala Leu Ala Ser  
1 5 10 15

Phe Ile Pro Leu His Ala His Ala Ser Ser Thr Ser Glu Asp Glu Met  
20 25 30

Ile Val Thr Gly Asn Thr Ala Ala Asp Thr Thr Asp Ser Ala Ala Gly  
35 40 45

Ala Gly Phe Lys Thr Asn Asp Ile Asp Val Gly Pro Leu Gly Thr Lys  
50 55 60

Ser Trp Ile Glu Thr Pro Tyr Ser Ser Thr Thr Val Thr Lys Glu Met  
65 70 75 80

Ile Glu Asn Gln Gln Ala Gln Ser Val Ser Glu Met Leu Lys Tyr Ser  
 85 90 95  
 Pro Ser Thr Gln Met Gln Ala Arg Gly Gly Met Asp Val Gly Arg Pro  
 100 105 110  
 Gln Ser Arg Gly Met Gln Gly Ser Val Val Ala Asn Ser Arg Leu Asp  
 115 120 125  
 Gly Leu Asn Ile Val Ser Thr Thr Ala Phe Pro Val Glu Met Leu Glu  
 130 135 140  
 Arg Met Asp Val Leu Asn Ser Leu Thr Gly Ala Leu Tyr Gly Pro Ala  
 145 150 155 160  
 Ser Pro Ala Gly Gln Phe Asn Phe Val Ala Lys Arg Pro Thr Glu Glu  
 165 170 175  
 Thr Leu Arg Lys Val Thr Leu Gly Tyr Gln Ser Arg Ser Ala Phe Thr  
 180 185 190  
 Gly His Ala Asp Leu Gly Gly His Phe Asp Glu Asn Lys Arg Phe Gly  
 195 200 205  
 Tyr Arg Val Asn Leu Leu Asp Gln Glu Gly Glu Gly Asn Val Asp Asp  
 210 215 220  
 Ser Thr Leu Arg Arg Lys Leu Val Ser Val Ala Leu Asp Trp Asn Ile  
 225 230 235 240  
 Gln Pro Gly Thr Gln Leu Gln Leu Asp Ala Ser His Tyr Glu Phe Ile  
 245 250 255  
 Gln Lys Gly Tyr Val Gly Ser Phe Asn Tyr Gly Pro Asn Val Lys Leu  
 260 265 270  
 Pro Ser Ala Pro Asn Pro Lys Asp Lys Asn Leu Ala Leu Ser Thr Ala  
 275 280 285  
 Gly Asn Asp Leu Thr Thr Asp Thr Ile Ser Thr Arg Leu Ile His Tyr  
 290 295 300  
 Phe Asn Asp Asp Trp Ser Met Asn Ala Gly Val Gly Trp Gln Gln Ala  
 305 310 315 320  
 Asp Arg Ala Met Arg Ser Val Ser Ser Lys Ile Leu Asn Asn Gln Gly  
 325 330 335  
 Asp Ile Ser Arg Ser Met Lys Asp Ser Thr Ala Ala Gly Arg Phe Arg  
 340 345 350

Val Leu Ser Asn Thr Ala Gly Leu Asn Gly His Ile Asp Thr Gly Ser  
355 360 365

Ile Gly His Asp Leu Ser Leu Ser Thr Thr Gly Tyr Val Trp Ser Leu  
370 375 380

Tyr Ser Ala Lys Gly Thr Gly Ser Ser Tyr Ser Trp Gly Thr Thr Asn  
385 390 395 400

Met Tyr His Pro Asp Ala Ile Asp Glu Gln Gly Asp Gly Lys Ile Arg  
405 410 415

Thr Gly Gly Pro Arg Tyr Arg Ser Ser Val Asn Thr Gln Gln Ser Val  
420 425 430

Thr Leu Gly Asp Thr Val Thr Phe Thr Pro Gln Trp Ser Ala Met Phe  
435 440 445

Tyr Leu Ser Gln Ser Trp Leu Gln Thr Lys Asn Tyr Asp Lys His Gly  
450 455 460

Asn Gln Thr Asn Gln Val Asp Glu Asn Gly Leu Ser Pro Asn Ala Ala  
465 470 475 480

Leu Met Tyr Lys Ile Thr Pro Asn Thr Met Ala Tyr Val Ser Tyr Ala  
485 490 495

Asp Ser Leu Glu Gln Gly Gly Thr Ala Pro Thr Asp Glu Ser Val Lys  
500 505 510

Asn Ala Gly Gln Thr Leu Asn Pro Tyr Arg Ser Lys Gln Tyr Glu Val  
515 520 525

Gly Leu Lys Ser Asp Ile Gly Glu Met Asn Leu Gly Ala Ala Leu Phe  
530 535 540

Arg Leu Glu Arg Pro Phe Ala Tyr Leu Asp Thr Asp Asn Val Tyr Lys  
545 550 555 560

Glu Gln Gly Asn Gln Val Asn Asn Gly Leu Glu Leu Thr Ala Ala Gly  
565 570 575

Asn Val Trp Gln Gly Leu Asn Ile Tyr Ser Gly Val Thr Phe Leu Asp  
580 585 590

Pro Lys Leu Lys Asp Thr Ala Asn Ala Ser Thr Ser Asn Lys Gln Val  
595 600 605

Val Gly Val Pro Lys Val Gln Ala Asn Leu Leu Ala Glu Tyr Ser Leu  
610 615 620

Pro Ser Ile Pro Glu Trp Val Tyr Ser Ala Asn Val His Tyr Thr Gly  
625 630 635 640

Lys Arg Ala Ala Asn Asp Thr Asn Thr Ser Tyr Ala Ser Ser Tyr Thr  
645 650 655

Thr Trp Asp Leu Gly Thr Arg Tyr Thr Thr Lys Val Ser Asn Val Pro  
660 665 670

Thr Thr Phe Arg Val Val Val Asn Asn Val Phe Asp Lys His Tyr Trp  
675 680 685

Ala Ser Ile Phe Pro Ser Gly Thr Asp Gly Asp Asn Gly Ser Pro Ser  
690 695 700

Ala Phe Ile Gly Gly Gly Arg Glu Val Arg Ala Ser Val Thr Phe Asp  
705 710 715 720

Phe

<210> 50 <211> 669 <212> PRT <213> Escherichia coli <400> 50

Met Lys Asn Ile Thr Leu Trp Gln Arg Leu Arg Gln Val Ser Ile Ser  
1 5 10 15

Thr Ser Leu Arg Cys Ala Phe Leu Met Gly Ala Leu Leu Thr Leu Ile  
20 25 30

Val Ser Ser Val Ser Leu Tyr Ser Trp His Glu Gln Ser Ser Gln Ile  
35 40 45

Arg Tyr Ser Leu Asp Lys Tyr Phe Pro Arg Ile His Ser Ala Phe Leu  
50 55 60

Ile Glu Gly Asn Leu Asn Leu Val Val Asp Gln Leu Asn Glu Phe Leu  
65 70 75 80

Gln Ala Pro Asn Thr Thr Val Arg Leu Gln Leu Arg Thr Gln Ile Ile  
85 90 95

Gln His Leu Asp Thr Ile Glu Arg Leu Ser Arg Gly Leu Ser Ser Arg  
100 105 110

Glu Arg Gln Gln Leu Thr Val Ile Leu Gln Asp Ser Arg Ser Leu Leu  
115 120 125

Ser Glu Leu Asp Arg Ala Leu Tyr Asn Met Phe Leu Leu Arg Glu Lys  
 130 135 140

Val Ser Glu Leu Ser Ala Arg Ile Asp Trp Leu His Asp Asp Phe Thr  
 145 150 155 160

Thr Glu Leu Asn Ser Leu Val Gln Asp Phe Thr Trp Gln Gln Gly Thr  
 165 170 175

Leu Leu Asp Gln Ile Ala Ser Arg Gln Gly Asp Thr Ala Gln Tyr Leu  
 180 185 190

Lys Arg Ser Arg Glu Val Gln Asn Glu Gln Gln Gln Val Tyr Thr Leu  
 195 200 205

Ala Arg Ile Glu Asn Gln Ile Val Asp Asp Leu Arg Asp Arg Leu Asn  
 210 215 220

Glu Leu Lys Ser Gly Arg Asp Asp Asp Ile Gln Val Glu Thr His Leu  
 225 230 235 240

Arg Tyr Phe Glu Asn Leu Lys Lys Thr Ala Asp Glu Asn Ile Arg Met  
 245 250 255

Leu Asp Asp Trp Pro Gly Thr Ile Thr Leu Arg Gln Thr Ile Asp Glu  
 260 265 270

Leu Leu Asp Met Gly Ile Val Lys Asn Lys Met Pro Asp Thr Met Arg  
 275 280 285

Glu Tyr Val Ala Ala Gln Lys Ala Leu Glu Asp Ala Ser Arg Thr Arg  
 290 295 300

Glu Ala Thr Gln Gly Arg Phe Arg Thr Leu Leu Glu Ala Gln Leu Gly  
 305 310 315 320

Ser Thr His Gln Gln Met Gln Met Phe Asn Gln Arg Met Glu Gln Ile  
 325 330 335

Val His Val Ser Gly Gly Leu Ile Leu Val Ala Thr Ala Leu Ala Leu  
 340 345 350

Leu Leu Ala Trp Val Phe Asn His Tyr Phe Ile Arg Ser Arg Leu Val  
 355 360 365

Lys Arg Phe Thr Leu Leu Asn Gln Ala Val Val Gln Ile Gly Leu Gly  
 370 375 380

Gly Thr Glu Thr Thr Ile Pro Val Tyr Gly Asn Asp Glu Leu Gly Arg  
 385 390 395 400



Ile Ala Gly Leu Leu Arg His Thr Leu Gly Gln Leu Asn Val Gln Lys  
 405 410 415  
 Gln Gln Leu Glu Gln Glu Ile Thr Asp Arg Lys Val Ile Glu Ala Asp  
 420 425 430  
 Leu Arg Ala Thr Gln Asp Glu Leu Ile Gln Thr Ala Lys Leu Ala Val  
 435 440 445  
 Val Gly Gln Thr Met Thr Thr Leu Ala His Glu Ile Asn Gln Pro Leu  
 450 455 460  
 Asn Ala Leu Ser Met Tyr Leu Phe Thr Ala Arg Arg Ala Ile Glu Gln  
 465 470 475 480  
 Thr Gln Lys Glu Gln Ala Ser Met Met Leu Gly Lys Ala Glu Gly Val  
 485 490 495  
 Ile Ser Arg Ile Asp Ala Ile Ile Arg Ser Leu Arg Gln Phe Thr Arg  
 500 505 510  
 Arg Ala Glu Leu Glu Thr Ser Leu His Ala Val Asp Leu Ala Gln Met  
 515 520 525  
 Phe Ser Ala Ala Trp Glu Leu Leu Ala Met Arg His Arg Ser Leu Gln  
 530 535 540  
 Ala Thr Leu Val Leu Pro Gln Gly Thr Ala Thr Val Ser Gly Asp Glu  
 545 550 555 560  
 Val Arg Thr Gln Gln Val Leu Val Asn Val Leu Ala Asn Ala Leu Asp  
 565 570 575  
 Val Cys Gly Gln Gly Ala Val Ile Thr Val Asn Trp Gln Met Gln Gly  
 580 585 590  
 Lys Thr Leu Asn Val Phe Ile Gly Asp Asn Gly Pro Gly Trp Pro Glu  
 595 600 605  
 Ala Leu Leu Pro Ser Leu Leu Lys Pro Phe Thr Thr Ser Lys Glu Val  
 610 615 620  
 Gly Leu Gly Ile Gly Leu Ser Ile Cys Val Ser Leu Met Glu Gln Met  
 625 630 635 640  
 Lys Gly Glu Leu Arg Leu Ala Ser Thr Met Thr Arg Asn Ala Cys Val  
 645 650 655

Val Leu Gln Phe Arg Leu Thr Asp Val Glu Asp Ala Lys  
660 665

<210> 51 <211> 753 <212> PRT <213> Escherichia coli <400> 51

Met Asn Val Ile Lys Leu Ala Ile Gly Ser Gly Ile Leu Leu Leu Ser  
1 5 10 15

Cys Gly Ala Tyr Ser Gln Ser Ile Ser Glu Lys Thr Asn Ser Asp Lys  
20 25 30

Lys Gly Ala Ala Glu Phe Ser Pro Leu Ser Val Ser Val Gly Lys Thr  
35 40 45

Thr Ser Glu Gln Glu Ala Leu Glu Lys Thr Gly Ala Thr Ser Ser Arg  
50 55 60

Thr Thr Asp Lys Asn Leu Gln Ser Leu Asp Ala Thr Val Arg Ser Met  
65 70 75 80

Pro Gly Thr Tyr Thr Gln Ile Asp Pro Gly Gln Gly Ala Ile Ser Val  
85 90 95

Asn Ile Arg Gly Met Ser Gly Phe Gly Arg Val Asn Thr Met Val Asp  
100 105 110

Gly Ile Thr Gln Ser Phe Tyr Gly Thr Ser Thr Ser Gly Thr Thr Thr  
115 120 125

His Gly Ser Thr Asn Asn Met Ala Gly Val Leu Ile Asp Pro Asn Leu  
130 135 140

Leu Val Ala Val Asp Val Thr Arg Gly Asp Ser Ser Gly Ser Glu Gly  
145 150 155 160

Ile Asn Ala Leu Ala Gly Ser Ala Asn Met Arg Thr Ile Gly Val Asp  
165 170 175

Asp Val Ile Phe Asn Gly Asn Thr Tyr Gly Leu Arg Ser Arg Phe Ser  
180 185 190

Val Gly Ser Asn Gly Leu Gly Arg Ser Gly Met Ile Ala Leu Gly Gly  
195 200 205

Lys Ser Asp Ala Phe Thr Asp Thr Gly Ser Ile Gly Val Met Ala Ala  
210 215 220

Val Ser Gly Ser Ser Val Tyr Ser Asn Phe Ser Asn Gly Ser Gly Ile  
225 230 235 240

Asn	Ser	Lys	Glu	Phe	Gly	Tyr	Asp	Lys	Tyr	Met	Lys	Gln	Asn	Pro	Lys
				245					250					255	
Ser	Gln	Leu	Tyr	Lys	Met	Asp	Ile	Arg	Pro	Asp	Glu	Phe	Asn	Ser	Phe
			260					265					270		
Glu	Leu	Ser	Ala	Arg	Thr	Tyr	Glu	Asn	Lys	Phe	Thr	Arg	Arg	Asp	Ile
		275					280					285			
Thr	Ser	Asp	Asp	Tyr	Tyr	Ile	Lys	Tyr	His	Tyr	Thr	Pro	Phe	Ser	Glu
	290					295					300				
Leu	Ile	Asp	Phe	Asn	Val	Thr	Ala	Ser	Thr	Ser	Arg	Gly	Asn	Gln	Lys
305					310					315					320
Tyr	Arg	Asp	Gly	Ser	Leu	Tyr	Thr	Phe	Tyr	Lys	Thr	Ser	Ala	Gln	Asn
				325					330					335	
Arg	Ser	Asp	Ala	Leu	Asp	Ile	Asn	Asn	Thr	Ser	Arg	Phe	Thr	Val	Ala
			340					345					350		
Asp	Asn	Asp	Leu	Glu	Phe	Met	Leu	Gly	Ser	Lys	Leu	Met	Arg	Thr	Arg
		355					360					365			
Tyr	Asp	Arg	Thr	Ile	His	Ser	Ala	Ala	Gly	Asp	Pro	Lys	Ala	Asn	Gln
	370					375					380				
Glu	Ser	Ile	Glu	Asn	Asn	Pro	Phe	Ala	Pro	Ser	Gly	Gln	Gln	Asp	Ile
385				390						395					400
Ser	Ala	Leu	Tyr	Thr	Gly	Leu	Lys	Val	Thr	Arg	Gly	Ile	Trp	Glu	Ala
				405					410					415	
Asp	Phe	Asn	Leu	Asn	Tyr	Thr	Arg	Asn	Arg	Ile	Thr	Gly	Tyr	Lys	Pro
			420					425					430		
Ala	Cys	Asp	Ser	Arg	Val	Ile	Cys	Val	Pro	Gln	Gly	Ser	Tyr	Asp	Ile
		435					440					445			
Asp	Asp	Lys	Glu	Gly	Gly	Phe	Asn	Pro	Ser	Val	Gln	Leu	Ser	Ala	Gln
	450					455					460				
Val	Thr	Pro	Trp	Leu	Gln	Pro	Phe	Ile	Gly	Tyr	Ser	Lys	Ser	Met	Arg
465				470					475						480
Ala	Pro	Asn	Ile	Gln	Glu	Met	Phe	Phe	Ser	Asn	Ser	Gly	Gly	Ala	Ser
				485					490					495	
Met	Asn	Pro	Phe	Leu	Lys	Pro	Glu	Arg	Ala	Glu	Thr	Trp	Gln	Ala	Gly
			500					505					510		

Phe Asn Ile Asp Thr Arg Asp Leu Leu Val Glu Gln Asp Ala Leu Arg  
 515 520 525  
 Phe Lys Ala Leu Ala Tyr Arg Ser Arg Ile Gln Asn Tyr Ile Tyr Ser  
 530 535 540  
 Glu Ser Tyr Leu Val Cys Ser Gly Gly Arg Lys Cys Ser Leu Pro Glu  
 545 550 555 560  
 Val Ile Gly Asn Gly Trp Glu Gly Ile Ser Asp Glu Tyr Ser Asp Asn  
 565 570 575  
 Met Tyr Ile Tyr Val Asn Ser Ala Ser Asp Val Ile Ala Lys Gly Phe  
 580 585 590  
 Glu Leu Glu Met Asp Tyr Asp Ala Gly Phe Ala Phe Gly Arg Leu Ser  
 595 600 605  
 Phe Ser Gln Gln Gln Thr Asp Gln Pro Thr Ser Ile Ala Ser Thr His  
 610 615 620  
 Phe Gly Ala Gly Asp Ile Thr Glu Leu Pro Arg Lys Tyr Met Thr Leu  
 625 630 635 640  
 Asp Thr Gly Val Arg Phe Phe Asp Asn Ala Leu Thr Leu Gly Thr Ile  
 645 650 655  
 Ile Lys Tyr Thr Gly Lys Ala Arg Arg Leu Ser Pro Asp Phe Glu Gln  
 660 665 670  
 Asp Glu His Thr Gly Ala Ile Ile Lys Gln Asp Leu Pro Gln Ile Pro  
 675 680 685  
 Thr Ile Ile Asp Leu Tyr Gly Thr Tyr Glu Tyr Asn Arg Asn Leu Thr  
 690 695 700  
 Leu Lys Leu Ser Val Gln Asn Leu Met Asn Arg Asp Tyr Ser Glu Ala  
 705 710 715 720  
 Leu Asn Lys Leu Asn Met Met Pro Gly Leu Gly Asp Glu Thr His Pro  
 725 730 735  
 Ala Asn Ser Ala Arg Gly Arg Thr Trp Ile Phe Gly Gly Asp Ile Arg  
 740 745 750  
 Phe

<210> 52 <211> 133 <212> PRT <213> Escherichia coli <400> 52

Met Ser Ser Lys Thr Lys Cys Trp Leu Trp Met Leu Leu Val Ile Leu  
1 5 10 15

Ser Glu Thr Ser Ala Thr Ser Thr Leu Lys Met Phe Asp Asn Ser Glu  
20 25 30

Gly Met Thr Lys Thr Leu Leu Leu Ala Leu Ile Val Val Leu Tyr Cys  
35 40 45

Ile Cys Tyr Tyr Ser Leu Ser Arg Ala Val Lys Asp Ile Pro Val Gly  
50 55 60

Leu Ala Tyr Ala Thr Trp Ser Gly Thr Gly Ile Leu Met Val Ser Thr  
65 70 75 80

Leu Gly Ile Leu Phe Tyr Gly Gln His Pro Asp Thr Ala Ala Ile Ile  
85 90 95

Gly Met Val Ile Ile Ala Ser Gly Ile Ile Ile Met Asn Leu Phe Ser  
100 105 110

Lys Met Gly Ser Glu Glu Ala Glu Glu Thr Pro Val Thr Asn Leu Asp  
115 120 125

Lys Lys Ile Ala Asn  
130

<210> 53 <211> 286 <212> PRT <213> Escherichia coli <400> 53

Met Tyr Ile Lys Lys His Trp Ile Ala Leu Ser Ile Leu Leu Ile Pro  
1 5 10 15

Cys Ile Gly Asn Ala Gln Glu Ile Lys Ile Asp Glu Ser Trp Leu His  
20 25 30

Gln Ser Leu Asn Val Ile Gly Arg Thr Asp Ser Arg Phe Gly Pro Arg  
35 40 45

Leu Thr Asn Asp Leu Tyr Pro Glu Tyr Thr Val Ala Gly Arg Lys Asp  
50 55 60

Trp Phe Asp Phe Tyr Gly Tyr Val Asp Leu Pro Lys Phe Phe Gly Val  
65 70 75 80

Gly Ser His Tyr Asp Val Gly Ile Trp Asp Glu Gly Ser Pro Leu Phe  
85 90 95

Thr Glu Ile Glu Pro Arg Phe Ser Ile Asp Lys Leu Thr Gly Leu Asn  
100 105 110

Leu Ala Phe Gly Pro Phe Lys Glu Trp Phe Ile Ala Asn Asn Tyr Val  
 115 120 125

Tyr Asp Met Gly Asp Asn Gln Ser Ser Arg Gln Ser Thr Trp Tyr Met  
 130 135 140

Gly Leu Gly Thr Asp Ile Asp Thr Gly Leu Pro Ile Lys Leu Ser Ala  
 145 150 155 160

Asn Ile Tyr Ala Lys Tyr Gln Trp Gln Asn Tyr Gly Ala Ala Asn Glu  
 165 170 175

Asn Glu Trp Asp Gly Tyr Arg Phe Lys Ile Lys Tyr Ser Ile Pro Leu  
 180 185 190

Thr Asn Leu Phe Gly Gly Arg Leu Val Tyr Asn Ser Phe Thr Asn Phe  
 195 200 205

Asp Phe Gly Ser Asp Leu Ala Asp Lys Ser His Asn Asn Lys Arg Thr  
 210 215 220

Ser Asn Ala Ile Ala Ser Ser His Ile Leu Ser Leu Leu Tyr Glu His  
 225 230 235 240

Trp Lys Phe Ala Phe Thr Leu Arg Tyr Phe His Asn Gly Gly Gln Trp  
 245 250 255

Asn Ala Gly Glu Lys Val Asn Phe Gly Asp Gly Pro Phe Glu Leu Lys  
 260 265 270

Asn Thr Gly Trp Gly Thr Tyr Thr Thr Ile Gly Tyr Gln Phe  
 275 280 285

<210> 54 <211> 172 <212> PRT <213> Escherichia coli <400> 54

Met Arg Ile Ala Pro Arg Thr Phe Phe Ala Ile Ser Ala Leu Ala Phe  
 1 5 10 15

Ile Val Ala Ser Gly Phe Ser Phe Trp Arg Leu Ser Pro Ala Glu Asn  
 20 25 30

Thr Gly Ile Met Ser Cys Ser Thr Lys Gly Ile Met Arg Phe Glu Asn  
 35 40 45

Met Glu Lys Glu Asn Val Asn Gly Asn Ile His Phe Asn Phe Gly Ser  
 50 55 60

Gln Gly Lys Gly Ser Met Val Leu Glu Gly Tyr Thr Asp Ser Ala Ala  
 65 70 75 80

Gly Trp Leu Tyr Leu Gln Arg Tyr Val Lys Phe Thr Tyr Thr Ser Lys  
85 90 95

Arg Val Ser Ala Thr Glu Arg His Tyr Arg Ile Ser Gln Trp Glu Ser  
100 105 110

Ser Ala Ser Ser Ile Asp Glu Ser Pro Asp Val Ile Phe Asp Tyr Phe  
115 120 125

Met Arg Glu Met Ser Asp Ser His Asp Gly Leu Phe Leu Asn Ala Gln  
130 135 140

Lys Leu Asn Asp Lys Ala Ile Leu Leu Ser Ser Ile Asn Ser Pro Leu  
145 150 155 160

Trp Ile Cys Thr Leu Lys Ser Gly Ser Lys Leu Asp  
165 170

<210> 55 <211> 182 <212> PRT <213> Escherichia coli <400> 55

Met Lys Ile Lys Val Ile Ala Leu Ala Thr Phe Val Ser Ala Val Phe  
1 5 10 15

Ala Gly Ser Ala Met Ala Tyr Asp Gly Thr Ile Thr Phe Thr Gly Lys  
20 25 30

Val Val Ala Gln Thr Cys Thr Val Asn Thr Ser Asp Lys Asp Leu Ala  
35 40 45

Val Thr Leu Pro Thr Val Ala Thr Ser Ser Leu Lys Asp Asn Ala Ala  
50 55 60

Thr Ser Gly Leu Thr Pro Phe Ala Ile Arg Leu Thr Gly Cys Ala Thr  
65 70 75 80

Gly Met Asn Ser Ala Gln Asn Val Lys Ala Tyr Phe Glu Pro Ser Ser  
85 90 95

Asn Ile Asp Leu Ala Thr His Asn Leu Lys Asn Thr Ala Thr Pro Thr  
100 105 110

Lys Ala Asp Asn Val Gln Ile Gln Leu Leu Asn Ser Asn Gly Thr Ser  
115 120 125

Thr Ile Leu Leu Gly Glu Ala Asp Asn Gly Gln Asp Val Gln Ser Glu  
130 135 140

Thr Ile Gly Ser Asp Gly Ser Ala Thr Leu Arg Tyr Met Ala Gln Tyr  
145 150 155 160

Tyr Ala Thr Gly Gln Ser Thr Ala Gly Asp Val Lys Ala Thr Val His  
 165 170 175

Tyr Thr Ile Ala Tyr Glu  
 180

<210> 56 <211> 359 <212> PRT <213> Escherichia coli <400> 56

Met Lys Arg Ile Phe Phe Ile Pro Leu Phe Leu Ile Leu Leu Pro Lys  
 1 5 10 15

Leu Ala Val Ala Gly Pro Asp Asp Tyr Val Pro Ser Gln Ile Ala Val  
 20 25 30

Asn Thr Ser Thr Leu Pro Gly Val Val Ile Gly Pro Ala Asp Ala His  
 35 40 45

Thr Tyr Pro Arg Val Ile Gly Glu Leu Ala Gly Thr Ser Asn Gln Tyr  
 50 55 60

Val Phe Asn Gly Gly Ala Ile Ala Leu Met Arg Gly Lys Phe Thr Pro  
 65 70 75 80

Ala Leu Pro Lys Ile Gly Ser Ile Thr Val Tyr Phe Pro Ser Arg Lys  
 85 90 95

Gln Arg Asp Ser Ser Asp Phe Asp Ile Tyr Asp Ile Gly Val Ser Gly  
 100 105 110

Leu Gly Ile Ile Ile Gly Met Ala Gly Tyr Trp Pro Ala Thr Pro Leu  
 115 120 125

Val Pro Ile Asn Ser Ser Gly Ile Tyr Ile Asp Pro Val Gly Ala Asn  
 130 135 140

Thr Asn Pro Asn Thr Tyr Asn Gly Ala Thr Ala Ser Phe Gly Ala Arg  
 145 150 155 160

Leu Phe Val Ala Phe Val Ala Thr Gly Arg Leu Pro Asn Gly Tyr Ile  
 165 170 175

Thr Ile Pro Thr Arg Gln Leu Gly Thr Ile Leu Leu Glu Ala Lys Arg  
 180 185 190

Thr Ser Leu Asn Asn Lys Gly Leu Thr Ala Pro Val Met Leu Asn Gly  
 195 200 205

Gly Arg Ile Gln Val Gln Ser Gln Thr Cys Thr Met Gly Gln Lys Asn  
 210 215 220



Tyr Val Val Pro Leu Asn Thr Val Tyr Gln Ser Gln Phe Thr Ser Leu  
225 230 235 240

Tyr Lys Glu Ile Gln Gly Gly Lys Ile Asp Ile His Leu Gln Cys Pro  
245 250 255

Asp Gly Ile Asp Val Tyr Ala Thr Leu Thr Asp Ala Ser Gln Pro Val  
260 265 270

Asn Arg Thr Asp Ile Leu Thr Leu Ser Ser Glu Ser Thr Ala Lys Gly  
275 280 285

Phe Gly Ile Arg Leu Tyr Lys Asp Ser Asp Val Thr Ala Ile Ser Tyr  
290 295 300

Gly Glu Asp Ser Pro Val Lys Gly Asn Gly Ser Gln Trp His Phe Ser  
305 310 315 320

Asp Tyr Arg Gly Glu Val Asn Pro His Ile Asn Leu Arg Ala Asn Tyr  
325 330 335

Ile Lys Ile Ala Asp Ala Thr Thr Pro Gly Ser Val Lys Ala Ile Ala  
340 345 350

Thr Ile Thr Phe Ser Tyr Gln  
355

<210> 57 <211> 844 <212> PRT <213> Escherichia coli <400> 57

Met Asn Ala Asn Asn Leu Ser Cys Leu Ile Tyr Cys Arg Cys Ser Leu  
1 5 10 15

Leu Leu Phe Ala Ala Leu Gly Leu Thr Val Thr Asn His Ser Phe Ala  
20 25 30

Ala Glu Glu Ala Glu Phe Asp Ser Glu Phe Leu His Leu Asp Lys Gly  
35 40 45

Ile Asn Ala Ile Asp Ile Arg Arg Phe Ser His Gly Asn Pro Val Pro  
50 55 60

Glu Gly Arg Tyr Tyr Ser Asp Ile Tyr Val Asn Asn Val Trp Lys Gly  
65 70 75 80

Lys Ala Asp Leu Gln Tyr Leu Arg Thr Ala Asn Thr Gly Ala Pro Thr  
85 90 95

Leu Cys Leu Thr Pro Glu Leu Leu Ser Leu Ile Asp Leu Val Lys Asp  
100 105 110

Thr Met Ser Gly Asn Thr Ser Cys Phe Pro Ala Ser Thr Gly Leu Ser  
 115 120 125

Ser Ala Arg Ile Asn Phe Asp Leu Ser Thr Leu Arg Leu Asn Ile Glu  
 130 135 140

Ile Pro Gln Ala Leu Leu Asn Thr Arg Pro Arg Gly Tyr Ile Ser Pro  
 145 150 155 160

Ala Gln Trp Gln Ser Gly Val Pro Ala Ala Phe Ile Asn Tyr Asp Ala  
 165 170 175

Asn Tyr Tyr Gln Tyr Ser Ser Ser Gly Thr Ser Asn Glu Gln Thr Tyr  
 180 185 190

Leu Gly Leu Lys Ala Gly Phe Asn Leu Trp Gly Trp Ala Leu Arg His  
 195 200 205

Arg Gly Ser Glu Ser Trp Asn Asn Ser Tyr Pro Ala Gly Tyr Gln Asn  
 210 215 220

Ile Glu Thr Ser Ile Met His Asp Leu Ala Pro Leu Arg Ala Gln Phe  
 225 230 235 240

Thr Leu Gly Asp Phe Tyr Thr Asn Gly Glu Leu Met Asp Ser Leu Ser  
 245 250 255

Leu Arg Gly Val Arg Leu Ala Ser Asp Glu Arg Met Leu Pro Gly Ser  
 260 265 270

Leu Arg Gly Tyr Ala Pro Ala Val Arg Gly Ile Ala Asn Ser Asn Ala  
 275 280 285

Lys Val Thr Ile Tyr Gln Asn Ala His Ile Leu Tyr Glu Thr Thr Val  
 290 295 300

Pro Ala Gly Pro Phe Val Ile Asn Asp Leu Tyr Pro Ser Gly Tyr Ala  
 305 310 315 320

Gly Asp Leu Leu Val Lys Ile Thr Glu Ser Asn Gly Gln Thr Arg Met  
 325 330 335

Phe Thr Val Pro Phe Ala Ala Val Ala Gln Leu Ile Arg Pro Gly Phe  
 340 345 350

Ser Arg Trp Gln Met Ser Val Gly Lys Tyr Arg Tyr Ala Asn Lys Thr  
 355 360 365

Tyr Asn Asp Leu Ile Ala Gln Gly Thr Tyr Gln Tyr Gly Leu Thr Asn  
 370 375 380  
 Asp Ile Thr Leu Asn Ser Gly Leu Thr Thr Ala Ser Gly Tyr Thr Ala  
 385 390 395 400  
 Gly Leu Ala Gly Leu Ala Phe Asn Thr Pro Leu Gly Ala Ile Ala Ser  
 405 410 415  
 Asp Ile Thr Leu Ser Arg Thr Ala Phe Arg Tyr Ser Gly Val Thr Arg  
 420 425 430  
 Lys Gly Tyr Ser Leu His Ser Ser Tyr Ser Ile Asn Ile Pro Ala Ser  
 435 440 445  
 Asn Thr Asn Ile Thr Leu Ala Ala Tyr Arg Tyr Ser Ser Lys Asp Phe  
 450 455 460  
 Tyr His Leu Lys Asp Ala Leu Ser Ala Asn His Asn Ala Phe Ile Asp  
 465 470 475 480  
 Asp Val Ser Val Lys Ser Thr Ala Phe Tyr Arg Pro Arg Asn Gln Phe  
 485 490 495  
 Gln Ile Ser Ile Asn Gln Glu Leu Gly Glu Lys Trp Gly Gly Met Tyr  
 500 505 510  
 Leu Thr Gly Thr Thr Tyr Asn Tyr Trp Gly His Lys Gly Ser Arg Asn  
 515 520 525  
 Glu Tyr Gln Ile Gly Tyr Ser Asn Phe Trp Lys Gln Leu Gly Tyr Gln  
 530 535 540  
 Ile Gly Leu Ser Gln Ser Arg Asp Asn Glu Gln Gln Arg Arg Asp Asp  
 545 550 555 560  
 Arg Phe Tyr Ile Asn Phe Thr Leu Pro Leu Gly Gly Ser Val Gln Ser  
 565 570 575  
 Pro Val Phe Ser Thr Val Leu Asn Tyr Ser Lys Glu Glu Lys Asn Ser  
 580 585 590  
 Ile Gln Thr Ser Ile Ser Gly Thr Gly Gly Glu Asp Asn Gln Phe Ser  
 595 600 605  
 Tyr Gly Ile Ser Gly Asn Ser Gln Glu Asn Gly Pro Ser Gly Tyr Ala  
 610 615 620  
 Met Asn Gly Gly Tyr Arg Ser Pro Tyr Val Asn Ile Thr Thr Thr Val  
 625 630 635 640

Gly His Asp Thr Gln Asn Asn Asn Gln Arg Ser Phe Gly Ala Ser Gly  
 645 650 655  
 Ala Val Val Ala His Pro Tyr Gly Val Thr Leu Ser Asn Asp Leu Ser  
 660 665 670  
 Asp Thr Phe Ala Ile Ile His Ala Glu Gly Ala Gln Gly Ala Val Ile  
 675 680 685  
 Asn Asn Ala Ser Gly Ser Arg Leu Asp Phe Trp Gly Asn Gly Val Val  
 690 695 700  
 Pro Tyr Val Thr Pro Tyr Glu Lys Asn Gln Ile Ser Ile Asp Pro Ser  
 705 710 715 720  
 Asn Leu Asp Leu Asn Val Glu Leu Ser Ala Thr Glu Gln Glu Ile Ile  
 725 730 735  
 Pro Arg Ala Asn Ser Ala Thr Leu Val Lys Phe Asp Thr Lys Thr Gly  
 740 745 750  
 Arg Ser Leu Leu Phe Asp Ile Arg Met Ser Thr Gly Asn Pro Pro Pro  
 755 760 765  
 Met Ala Ser Glu Val Leu Asp Glu His Gly Gln Leu Ala Gly Tyr Val  
 770 775 780  
 Ala Gln Ala Gly Lys Val Phe Thr Arg Gly Leu Pro Glu Lys Gly His  
 785 790 795 800  
 Leu Ser Val Val Trp Gly Pro Asp Asn Lys Asp Arg Cys Ser Phe Val  
 805 810 815  
 Tyr His Val Ala His Asn Lys Asp Asp Met Gln Ser Gln Leu Val Pro  
 820 825 830  
 Val Leu Cys Ile Gln His Pro Asn Gln Glu Lys Thr  
 835 840  
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 Ile Val Phe Ile Val Leu Ile Gly Trp Ile Ile Phe Arg Pro Lys Ala  
 20 25 30  
 Tyr Thr Tyr Ser Leu Asn Asp Lys Glu Lys Glu Met Leu Ile Met Leu  
 35 40 45

Ser Gln His Pro Glu Thr Arg Tyr Phe Gly Phe Tyr Ser Ile Glu Leu  
50 55 60

Pro Ala Asp Tyr Lys Pro Thr Gly Met Val Met Phe Ile Gln Gly Ser  
65 70 75 80

Ala Met Ile Pro Val Glu Thr Lys Leu Gln Tyr Tyr Pro Pro Phe Leu  
85 90 95

Gln Tyr Met Thr Arg Tyr Glu Ala Glu Leu Lys Asn Thr Ser Ala Leu  
100 105 110

Asp Pro Leu Asp Thr Pro Tyr Leu Lys Gln Val His Pro Leu Ser Pro  
115 120 125

Pro Met Asn Gly Val Ile Phe Glu Arg Met Lys Ala Lys Tyr Thr Pro  
130 135 140

Asp Phe Ala Arg Val Leu Asp Ala Trp Lys Trp Glu Asn Gly Val Thr  
145 150 155 160

Phe Ser Val Lys Ile Glu Ala Lys Asp Gly Arg Ala Thr Arg Tyr Asp  
165 170 175

Gly Ile Ser Lys Ile Ala Glu Tyr Ser Tyr Gly Tyr Asn Ile Pro Glu  
180 185 190

Lys Lys Val Gln Leu Leu Thr Ile Leu Ser Gly Leu Gln Pro Arg Ala  
195 200 205

Asp Asn Gln Pro Pro Ser Glu Asn Lys Leu Ala Ile Gln Tyr Ala Gln  
210 215 220

Val Asp Ala Ser Leu Leu Gly Glu Tyr Glu Leu Ser Val Asp Tyr Lys  
225 230 235 240

Asn Ser Asn Asn Ile Lys Ile Ser Leu Gln Thr Asp Asn Asn Ser Tyr  
245 250 255

Ile Asp Ser Leu Leu Asp Ile Arg Tyr Pro Ser Asn Gly Asn Arg Ala  
260 265 270

Trp Tyr Asn Ser Ile  
275

<210> 59 <211> 366 <212> PRT <213> Escherichia coli <400> 59

Met Leu Pro Glu Pro Val Tyr Arg Arg Trp Ile Ile Leu Leu Ile Ser  
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Met Leu Thr Val Gly Thr Leu Phe Ile Leu Ser Val Trp Asn Ser Ala  
 20 25 30  
 Thr Tyr Trp Asp Ile Phe Ile Tyr Gly Val Leu Pro Met Leu Phe Leu  
 35 40 45  
 Trp Leu Cys Leu Phe Gly Ile Ala Leu Asn Lys Tyr Glu Gln Ser Val  
 50 55 60  
 Ala Ala Cys Ile Ser Trp Glu Ser Glu Arg Gln Gln Val Lys Gln Leu  
 65 70 75 80  
 Trp Gln His Trp Ser Gln Lys Gln Leu Ala Ile Val Gly Asn Val Leu  
 85 90 95  
 Phe Thr Pro Glu Glu Lys Gly Met Ser Val Leu Leu Gly Pro Gln Glu  
 100 105 110  
 Glu Ile Pro Ala Tyr Pro Lys Lys Ala Arg Pro Leu Phe Ser Ala Ser  
 115 120 125  
 Arg Tyr Ser Leu Ser Ser Ile Phe His Asp Ile His Gln Gln Leu Thr  
 130 135 140  
 Gln Gln Phe Pro Asp Tyr Arg His Tyr Leu His Thr Ile Tyr Val Leu  
 145 150 155 160  
 Gln Pro Glu Lys Trp Arg Gly Glu Thr Val Arg Gln Ala Ile Phe His  
 165 170 175  
 Gln Trp Asp Leu Val Pro Glu Arg Thr Asn Thr Leu Asn Gln Ile Gln  
 180 185 190  
 Ser Leu Tyr Asp Glu Arg Phe Asp Gly Leu Ile Leu Val Val Cys Leu  
 195 200 205  
 Gln Asn Trp Pro Glu Asn Lys Pro Glu Asp Thr Ser Glu Leu Val Ser  
 210 215 220  
 Ala Gln Leu Ile Ser Ser Ser Ser Phe Val Arg Gln His Gln Ile Pro  
 225 230 235 240  
 Val Ile Ala Gly Leu Gly Arg Val Met Pro Leu Glu Pro Glu Glu Leu  
 245 250 255  
 Glu His Asn Leu Asp Val Leu Phe Glu Tyr Asn Gln Leu Asp Asn Lys  
 260 265 270

Gln Leu Gln His Val Trp Val Ser Gly Leu Asp Glu Gly Thr Ile Glu  
275 280 285

Asn Leu Met Gln Tyr Ala Glu Gln His Gln Trp Ser Leu Pro Lys Lys  
290 295 300

Arg Pro Leu His Met Ile Asp His Ser Phe Gly Pro Thr Gly Glu Phe  
305 310 315 320

Ile Phe Pro Val Ser Leu Ala Met Leu Ser Glu Ala Ala Lys Glu Thr  
325 330 335

Glu Gln Asn His Leu Ile Ile Tyr Gln Ser Ala Gln Tyr Ala Gln Lys  
340 345 350

Lys Ser Leu Cys Leu Ile Thr Arg Lys Leu Tyr Leu Arg Thr  
355 360 365

<210> 60 <211> 260 <212> PRT <213> Escherichia coli <400> 60

Met Leu Asn Arg Lys Leu Asn Ile Arg Leu Arg His Ser Leu Asn Ser  
1 5 10 15

His Cys Ile Pro Ser Ile Ile Ile Asn Asn Thr Val Arg Ser Phe Gln  
20 25 30

Arg Ser Val Met Asn Thr Arg Ala Leu Phe Pro Leu Leu Phe Thr Val  
35 40 45

Ala Ser Phe Ser Ala Ser Ala Gly Asn Trp Ala Val Lys Asn Gly Trp  
50 55 60

Cys Gln Thr Met Thr Glu Asp Gly Gln Ala Leu Val Met Leu Lys Asn  
65 70 75 80

Gly Thr Ile Gly Ile Thr Gly Leu Met Gln Gly Cys Pro Asn Gly Val  
85 90 95

Gln Thr Leu Leu Gly Ser Arg Ile Ser Ile Asn Gly Asn Leu Ile Pro  
100 105 110

Thr Ser Gln Met Cys Asn Gln Gln Thr Gly Phe Arg Ala Val Glu Val  
115 120 125

Glu Ile Gly Gln Ala Pro Glu Met Val Lys Lys Ala Val His Ser Ile  
130 135 140

Ala Glu Arg Asp Val Ser Val Leu Gln Ala Phe Gly Val Arg Met Glu  
145 150 155 160

Phe Thr Arg Gly Asp Met Leu Lys Val Cys Pro Lys Phe Val Thr Ser  
 165 170 175  
 Leu Ala Gly Phe Ser Pro Lys Gln Thr Thr Thr Ile Asn Lys Asp Ser  
 180 185 190  
 Val Leu Gln Ala Ala Arg Gln Ala Tyr Ala Arg Glu Tyr Asp Glu Glu  
 195 200 205  
 Thr Thr Glu Thr Ala Asp Phe Gly Ser Tyr Glu Val Lys Gly Asn Lys  
 210 215 220  
 Val Glu Phe Glu Val Phe Asn Pro Glu Asp Arg Ala Tyr Asp Lys Val  
 225 230 235 240  
 Thr Val Thr Val Gly Ala Asp Gly Asn Ala Thr Gly Ala Ser Val Glu  
 245 250 255  
 Phe Ile Gly Lys  
 260  
 <210> 61 <211> 385 <212> PRT <213> Escherichia coli <400> 61  
 Val Val Ile Ile Asn Ser Thr Ile Leu Ser Gly Ala Gly Ala Ile Pro  
 1 5 10 15  
 Ser Leu Thr Ser Leu Leu Pro Asp Ile Arg Lys Met Leu Leu Val Thr  
 20 25 30  
 Asp Arg Asn Ile Ala Gln Leu Asp Gly Val Gln Gln Ile Arg Ala Leu  
 35 40 45  
 Leu Glu Lys His Cys Pro Gln Val Asn Val Ile Asp Asn Val Pro Ala  
 50 55 60  
 Glu Pro Thr His His Asp Val Arg Gln Leu Met Asp Ala Pro Gly Asp  
 65 70 75 80  
 Ala Ser Phe Asp Val Val Val Gly Ile Gly Gly Gly Ser Val Leu Asp  
 85 90 95  
 Val Ala Lys Leu Leu Ser Val Leu Cys His Pro Gln Ser Pro Gly Leu  
 100 105 110  
 Asp Ala Leu Leu Ala Gly Glu Lys Pro Thr Gln Arg Val Gln Ser Trp  
 115 120 125  
 Leu Ile Pro Thr Thr Ala Gly Thr Gly Ser Glu Ala Thr Pro Asn Ala  
 130 135 140



Ile Leu Ala Ile Pro Glu Gln Ser Thr Lys Val Gly Ile Ile Ser Gln  
 145 150 155 160

Val Leu Leu Pro Asp Tyr Val Ala Leu Phe Pro Glu Leu Thr Thr Ser  
 165 170 175

Met Pro Ala His Ile Ala Ala Ser Thr Gly Ile Asp Ala Leu Cys His  
 180 185 190

Leu Leu Glu Cys Phe Thr Ala Thr Val Ala Asn Pro Val Ser Asp Asn  
 195 200 205

Ala Ala Leu Thr Gly Leu Ser Lys Leu Phe Arg His Ile Gln Pro Ala  
 210 215 220

Val Asn Asp Pro Gln Asp Leu Arg Ala Lys Leu Glu Met Leu Trp Ala  
 225 230 235 240

Ser Tyr Tyr Gly Gly Val Ala Ile Thr His Ala Gly Thr His Leu Val  
 245 250 255

His Ala Leu Ser Tyr Pro Leu Gly Gly Lys Tyr His Leu Pro His Gly  
 260 265 270

Val Ala Asn Ala Ile Leu Leu Ala Pro Cys Met Ala Phe Val Arg Pro  
 275 280 285

Trp Ala Val Glu Lys Phe Ala Arg Val Trp Asp Cys Ile Pro Asp Ala  
 290 295 300

Glu Thr Ala Leu Ser Ala Glu Glu Lys Ser His Ala Leu Val Thr Trp  
 305 310 315 320

Leu Gln Ala Leu Val Asn Gln Leu Lys Leu Pro Asn Asn Leu Ala Ala  
 325 330 335

Leu Gly Val Pro Pro Glu Asp Ile Ala Ser Leu Ser Glu Ala Ala Leu  
 340 345 350

Asn Val Lys Arg Leu Met Asn Asn Val Pro Cys Gln Ile Asp Leu Gln  
 355 360 365

Asp Val Gln Ala Ile Tyr Gln Thr Leu Phe Pro Gln His Pro Phe Lys  
 370 375 380

Glu  
 385

<210> 62 <211> 105 <212> PRT <213> Escherichia coli <400> 62

Met Asn Ile Arg Lys Leu Phe Cys Pro Gly Asn Thr Pro Arg Ile Leu  
1 5 10 15

Leu Phe Leu Phe Phe Phe Val Val Ser Ala Ile Thr Thr Ile Ala Cys  
20 25 30

Gly Tyr Thr Glu Lys Asn Ala Thr Gly Asn Val Leu Leu Leu Phe Leu  
35 40 45

Leu Leu Leu Leu Ala His Arg Asn Thr Leu Thr Ser Ile Thr Ala Leu  
50 55 60

Leu Phe Leu Phe Cys Cys Ala Leu Tyr Ala Pro Ala Gly Met Thr Tyr  
65 70 75 80

Gly Lys Ile Asn Asn Ser Phe Ile Val Ala Leu Leu Gln Thr Thr Thr  
85 90 95

Asp Glu Ala Ala Glu Phe Thr Gly Met  
100 105

<210> 63 <211> 147 <212> PRT <213> Escherichia coli <400> 63

Met Asn Ile Gln Ala Ile Lys Glu Met Val Asn Leu Ile Cys Ser Phe  
1 5 10 15

Leu Phe Ile Phe Phe Leu Ser Ser Ala Phe Val Ser Phe Gly Cys Tyr  
20 25 30

Ala Ile Tyr Glu Leu Phe Leu Trp Asn Asp Ile Ile Val Tyr Ser Trp  
35 40 45

Gly Tyr Ile Leu Ile Val Phe Leu Pro Phe Thr Leu Tyr Val Met Ser  
50 55 60

Phe Glu Ile Leu Phe Phe Ala Ile Ser Gly Arg Arg Leu Ser Lys Val  
65 70 75 80

Thr Met Val Arg Leu Trp Leu Ile Ile Lys Ile Ile Ile Ala Phe Ser  
85 90 95

Ile Cys Ala Val Leu Ile Phe Ser Ser Ile Tyr Lys Lys Glu Leu Leu  
100 105 110

Ser Arg Asn Tyr Ile Ala Cys Ser Gly Ile Pro Ser Gly Trp Met Pro  
115 120 125

Gly Leu Ala Thr Lys Tyr Val Lys Glu Lys Ser Leu Cys Glu Lys Asn  
130 135 140

Gly Asn Asn  
145

<210> 64 <211> 178 <212> PRT <213> Escherichia coli <400> 64

Met Phe Pro Ile Arg Phe Lys Arg Pro Ala Leu Leu Cys Met Ala Met  
1 5 10 15

Leu Thr Val Val Leu Ser Gly Cys Gly Leu Ile Gln Lys Val Val Asp  
20 25 30

Glu Ser Lys Ser Val Ala Ser Ala Val Phe Tyr Lys Gln Ile Lys Ile  
35 40 45

Leu His Leu Asp Phe Phe Ser Arg Ser Ala Leu Asn Thr Asp Ala Glu  
50 55 60

Asp Thr Pro Leu Ser Thr Met Val His Val Trp Gln Leu Lys Thr Arg  
65 70 75 80

Glu Asp Phe Asp Lys Ala Asp Tyr Asp Thr Leu Phe Met Gln Glu Glu  
85 90 95

Lys Thr Leu Glu Lys Asp Val Leu Ala Lys His Thr Val Trp Val Lys  
100 105 110

Pro Glu Gly Thr Ala Ser Leu Asn Val Pro Leu Asp Lys Glu Thr Gln  
115 120 125

Phe Val Ala Ile Ile Gly Gln Phe Tyr His Pro Asp Glu Lys Ser Asp  
130 135 140

Ser Trp Arg Leu Val Ile Lys Arg Asp Glu Leu Glu Ala Asp Lys Pro  
145 150 155 160

Arg Ser Ile Glu Leu Met Arg Ser Asp Leu Arg Leu Leu Pro Leu Lys  
165 170 175

Asp Lys

<210> 65 <211> 209 <212> PRT <213> Escherichia coli <400> 65

Met Phe Leu Lys Arg Lys Trp Tyr Tyr Ala Val Thr Thr Ser Val Val  
1 5 10 15

Ile Thr Leu Cys Gly Gly Gly Tyr Tyr Met Tyr Arg Gln Glu Tyr Gln  
20 25 30

Met Val Val Thr Val Pro Thr Ala Asp Ala Asn Asp Pro Asn Trp Pro  
35 40 45

Asn Lys Arg Ile Gln Phe Asp Thr Ser Glu Trp Leu Gln Gln Leu Gln  
 50 55 60  
 Tyr Ile Lys Ile Asp Asp His Tyr Ile Leu Asn Thr Gln Tyr Thr Pro  
 65 70 75 80  
 Ile Ala Asn Leu Asp Asp Phe Gly Ile Thr Leu Lys Leu Gln Asn Ala  
 85 90 95  
 Leu Asn Gly Ser Asp Lys Arg Leu Pro Ala Leu Tyr Gly Leu Ala Glu  
 100 105 110  
 Met Asp Ala Gln Lys Phe Lys Asp Leu Met Arg Gly Lys Ile Lys Cys  
 115 120 125  
 Glu Tyr Leu Arg Thr Thr Phe Asp Ala Glu Thr Leu Lys Pro Val Asn  
 130 135 140  
 Asp Tyr Phe Leu Ile Ser Phe Thr Tyr Lys Asp Lys Trp Tyr Glu Phe  
 145 150 155 160  
 Glu Thr Glu Arg Lys Ile Ser Lys Thr Ser Asp Asp Gly Tyr Phe Leu  
 165 170 175  
 Trp Ala Phe Asp Asn Thr Val His Glu Ala Gly Tyr Trp His Asn Thr  
 180 185 190  
 Asp Pro Ala Ala Tyr Ser Tyr Arg Asp Tyr Gln Asn Gly Lys Ala Val  
 195 200 205  
 Lys  
 <210> 66 <211> 424 <212> PRT <213> Escherichia coli <400> 66  
 Met Asp Ile Trp Arg Gly His Ser Phe Leu Met Thr Ile Ser Ala Arg  
 1 5 10 15  
 Phe Arg Gln Tyr Val Phe Ser Leu Met Ser Ile Leu Leu Gln Glu Arg  
 20 25 30  
 Lys Met Asn Ile Phe Thr Leu Ser Lys Ala Pro Leu Tyr Leu Leu Ile  
 35 40 45  
 Ser Leu Phe Leu Pro Thr Met Ala Met Ala Ile Asp Pro Pro Glu Arg  
 50 55 60  
 Glu Leu Ser Arg Phe Ala Leu Lys Thr Asn Tyr Leu Gln Ser Pro Asp  
 65 70 75 80

Glu	Gly	Val	Tyr	Glu	Leu	Ala	Phe	Asp	Asn	Ala	Ser	Lys	Lys	Val	Phe	
				85					90						95	
Ala	Ala	Val	Thr	Asp	Arg	Val	Asn	Arg	Glu	Ala	Asn	Lys	Gly	Tyr	Leu	
			100					105					110			
Tyr	Ser	Phe	Asn	Ser	Asp	Ser	Leu	Lys	Val	Glu	Asn	Lys	Tyr	Thr	Met	
		115					120					125				
Pro	Tyr	Arg	Ala	Phe	Ser	Leu	Ala	Ile	Asn	Gln	Asp	Lys	His	Gln	Leu	
	130					135					140					
Tyr	Ile	Gly	His	Thr	Gln	Ser	Ala	Ser	Leu	Arg	Ile	Ser	Met	Phe	Asp	
145					150					155					160	
Thr	Pro	Thr	Gly	Lys	Leu	Val	Arg	Thr	Ser	Asp	Arg	Leu	Ser	Phe	Lys	
				165					170					175		
Ala	Ala	Asn	Ala	Ala	Asp	Ser	Arg	Phe	Glu	His	Phe	Arg	His	Met	Val	
			180					185					190			
Tyr	Ser	Gln	Asp	Ser	Asp	Thr	Leu	Phe	Val	Ser	Tyr	Ser	Asn	Met	Leu	
		195					200					205				
Lys	Thr	Ala	Glu	Gly	Met	Lys	Pro	Leu	His	Lys	Leu	Leu	Met	Leu	Asp	
	210					215					220					
Gly	Thr	Thr	Leu	Ala	Leu	Lys	Gly	Glu	Val	Lys	Asp	Ala	Tyr	Lys	Gly	
225					230					235					240	
Thr	Ala	Tyr	Gly	Leu	Thr	Met	Asp	Glu	Lys	Thr	Gln	Lys	Ile	Tyr	Val	
				245					250					255		
Gly	Gly	Arg	Asp	Tyr	Ile	Asn	Glu	Ile	Asp	Ala	Lys	Asn	Gln	Thr	Leu	
			260					265					270			
Leu	Arg	Thr	Ile	Pro	Leu	Lys	Asp	Pro	Arg	Pro	Gln	Ile	Thr	Ser	Val	
		275					280					285				
Gln	Asn	Leu	Ala	Val	Asp	Ser	Ala	Ser	Asp	Arg	Ala	Phe	Val	Val	Val	
	290					295					300					
Phe	Asp	His	Asp	Asp	Arg	Ser	Gly	Thr	Lys	Asp	Gly	Leu	Tyr	Ile	Phe	
305					310					315					320	
Asp	Leu	Arg	Asp	Gly	Lys	Gln	Leu	Gly	Tyr	Val	His	Thr	Gly	Ala	Gly	
				325					330					335		

Ala Asn Ala Val Lys Tyr Asn Pro Lys Tyr Asn Glu Leu Tyr Val Thr  
 340 345 350

Asn Phe Thr Ser Gly Thr Ile Ser Val Val Asp Ala Thr Lys Tyr Ser  
 355 360 365

Ile Thr Arg Glu Phe Asn Met Pro Val Tyr Pro Asn Gln Met Val Leu  
 370 375 380

Ser Asp Asp Met Asp Thr Leu Tyr Ile Gly Ile Lys Glu Gly Phe Asn  
 385 390 395 400

Arg Asp Trp Asp Pro Asp Val Phe Val Glu Gly Ala Lys Glu Arg Ile  
 405 410 415

Leu Ser Ile Asp Leu Lys Lys Ser  
 420

<210> 67 <211> 489 <212> DNA <213> Escherichia coli <400> 67  
 atgaaactga aagctattat attggccacc ggtcttatta actgtattgt attttcagca 60  
 caggcagtgg atacgacgat tactgtgacg ggtaatgttt tgcaaagaac atgtaatgta 120  
 ccagggaatg tggatgtttc tttgggtaat ctgtatgtat cagactttcc caatgcagga 180  
 agtggatctc catgggttaa ttttgatctg tctctcaccg gatgccagaa tatgaatact 240  
 gttcgggcaa catttagtgg tactgoggat gggcagacat actatgcgaa tacagggaat 300  
 gctggcggta tcaagattga aattcaggac agggatggaa gtaatgcatc atatcacaat 360  
 ggtatgttca agacgcttaa tgtacaaaat aataatgcaa cctttaatct taaagcccgt 420  
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 acctatgcg 489

<210> 68 <211> 2019 <212> DNA <213> Escherichia coli <400> 68  
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 aatgcccaga cttcacagca agacgaaagc acgctggtgg ttaccgccag taaacaatct 120  
 tccgcctcgg catcagccaa caacgtctcg tctactgttg tcagcgcgcc ggaattaagc 180  
 gacgccggcg tcaccgccag cgacaaactc cccagagtct tgcccgggct caatattgaa 240  
 aatagcggca acatgctttt ttgcacgacg tcgctacgcg gcgtctcttc agcgcaggac 300  
 ttctataacc ccgccgtcac cctgtatgtc gatggcgtcc ctcagctttc caccaacacc 360  
 atccaggcgc ttaccgatgt gcaaagcgtg gagttgctgc gaggcccaca gggaacgtta 420  
 tatggcaaaa gcgctcaggg cgggatcatc aacatcgtca cccagcagcc ggacagcacg 480  
 ccgcgcggct atattgaagg gcgcgtcagt agccgcgaca gttatcgaag taagttcaac 540  
 ctgagcggcc ccattcagga tggcctgctg tacggcagcg tcaccctgtt acgccagggt 600  
 gatgacggcg acatgattaa ccccgcgacg ggaagcgatg acttaggcgg caccgcgcc 660

agcatagggga atgtgaaact gcgtctggcg ccggacgac agccctggga aatgggcttt 720  
 gccgcctcac gcgaatgtac ccgcgccacc caggacgcct atgtgggatg gaatgatatt 780  
 aagggccgta agctgtcgat cagcgatggg tcaccagacc cgtacatgcg gcgctgcact 840  
 gacagccaga ccctgagtgg gaaatacacc accgatgact gggttttcaa cctgatcagc 900  
 gcctggcagc agcagcatta ttccgcgacc ttcccttcgc gttcgttaat cgtcaatatg 960  
 tctcagcgct ggaatcagga tgtgcaggag ctgcgcgctg caaccctggg cgatgcgcgt 1020  
 accgttgata tgggtgtttg gctgtaccgg cagaacaccc gcgagaagtt aaattcagcc 1080  
 tacgacatgc cgacaatgcc ttatttaagc agtaccggct ataccaccgc tgaaacgctg 1140  
 gccgcataca gtgacctgac ctggcattta accgatcggt ttgatatcgg cggcggcggtg 1200  
 cgcttctcgc atgataaatc cagtacacaa tatcaaggca gcatgctcgg caaccggttt 1260  
 ggcgaccagg gtaagagcaa tgacgatcag gtgctcgggc agctatccgc aggtatatg 1320  
 ctgaccgatg actggagagt gtatacccggt gtagcccgagg gatataaacc ttccgggtac 1380  
 aacatcgctg ctactgcggg tcttgatgcc aaaccgttcg tcgccgagaa atccatcaac 1440  
 tatgaacttg gcaccgcgta cgaaaccgct gacgtcacgc tgcaagccgc gacgttttat 1500  
 acccacacca aagacatgca gctttactct ggcccggtcg ggatgcagac attaagcaat 1560  
 gcgggtaaaag ccgacgccac cggcggttgag cttgaagcga agtggcggtt tgcgccaggc 1620  
 tggatcatggg atatcaatgg caacgtgatc cgttccgaat tcaccaatga cagtgaattg 1680  
 tatcacggtg accgggtgcc gttcgtacca cgttatggcg cgggaagcag cgtgaacggc 1740  
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ttcaccgcg	gtgatatgct	gaaggctctg	ccgaaatttg	tcacatcact	tgccggtttt	540
tccccgaaac	agacgaccac	tattaataaa	gattccgtcc	tgcaggctgc	ccggcaggca	600
tacgcccg	aatatgaaga	ggaaacaaca	gaaaccgctg	attttggctc	ttacgaagta	660
aaaggcaata	aggttgagtt	tgaagtattc	aatcctgaag	accgtgcgta	cgacaaagtg	720
accgtcacgg	ttgggtgctga	cggtaatgcc	accggcgcca	gcgttgaatt	tatcggaaaa	780
 <210> 127 <211> 1155 <212> DNA <213> Escherichia coli <400> 127						
gtggtaatta	tcaatagcac	gatactgagc	ggcgcaggcg	ctatcccttc	cctgacgtcg	60
ctcttaccgg	acatcagaaa	aatgctgctg	gtcactgacc	gtaatatgtc	gcagctcgac	120
ggtgtgcagc	agattcgcg	cttactggaa	aagcactgcc	cgcagggtta	cgttatcgat	180
aatgtgccc	cagagcccac	gcacatgat	gtgcgccagc	taatggatgc	ccctggcgat	240
gcctcttttg	atgtgggtgg	cgggatccgc	ggtggcagcg	tggtggatgt	ggcgaagctg	300
ctatcgggtg	tttgccatcc	acaatcaccg	gggctggatg	cgctgcttgc	gggtgaaaaa	360
ccgactcagc	gggtgcaatc	atgggttgatt	cctacaaccg	ccggaaccgg	ctcagaagcc	420
acgccgaatg	cgattctggc	aatccctgag	caaagcacga	aggtgggtat	tatttcccag	480
gtgctgttac	cagactatgt	ggcgcttttc	ccggaactga	ccaccagcat	gcccgcgcat	540
attgcggcgt	ccacgggcat	tgatgctctt	tgccacttac	tggagtgttt	taccgcgacc	600
gtggcaaatc	cggtcagcga	taacgcggcg	ctgactgggt	taagtaaact	tttccggcac	660
attcaaccgg	ccgtgaacga	tcctcaggat	ctgcgcgcaa	aaactggaaat	gctgtgggcg	720
tcttactatg	gcggcgtagc	gataacccat	gcgggcacgc	atctcgttca	tgcgctctcc	780
tacccgttag	gtggcaaata	tcactctgcc	catggcgctc	cgaatgccat	cttgctggcg	840
ccgtgcatgg	cgtttggttc	cccctgggcg	gtcgagaaat	ttgcccgggt	ctgggattgc	900
attcccgatg	cggaaccgc	cctgagcgcg	gaagaaaaat	ctcatgccct	ggtgacctgg	960
ttacaggcat	tagtcaatca	actcaagcta	cccaacaatc	tcgcggctct	cggcgtagcc	1020
ccagaggata	ttgcctctct	gagcgaggcg	gcactgaacg	tgaagcgcct	tatgaacaat	1080
gtgccgtgcc	aaattgatct	acaggacgta	caggccattt	accaaact	gtttccgcaa	1140
catccattta	aggag					1155

<210> 128 <211> 315 <212> DNA <213> Escherichia coli <400> 128  
 atgaatatca gaaaactggt ttgtccggga aacaccccc ggattttatt gtttttattc 60  
 ttttttgttg tttctgcaat aaccacaatt gcatgcggat acactgagaa gaatgcaaca 120  
 ggaaatgtgc tgcttctgtt tctccttctg ctccttgac acagaaatac cctcacatcc 180  
 attacagcgc tgttatttct gttctgttgt gcaactgtatg cgcctgccgg tatgacgtac 240  
 ggtaaaatca acaacagttt tattgtcgcg ttgttgacaga ccacaactga tgaggcagcg 300  
 gagtttaccg ggatg 315

<210> 129 <211> 441 <212> DNA <213> Escherichia coli <400> 129  
 atgaatatc aggcaataaa agaatggta aatttaattt gtagtttttt atttatattc 60  
 tttctgtcct cggcttttgt ttcttttggg tgttatgcta tttatgaatt gtttttatgg 120  
 aatgatatta ttgtatatag ctggggatat atattaattg tctttttacc tttcacatta 180  
 tatgtaatgt cgtttgagat tttgtttttt gctatttagt ggcgacgatt gtctaaagta 240  
 acaatgggtgc gcctttggtt gataattaaa attattattg ctttctctat ttgcgcagtg 300  
 ttgatttttt cttcaattta caaaaaagaa ttattatcta gaaattatat tgctttagt 360  
 ggtatcccg tgggtggat gccgggtctg gcaacgaaat acgttaaaga aaaatcatta 420  
 tgcgaaaaaa atggcaataa t 441

<210> 130 <211> 534 <212> DNA <213> Escherichia coli <400> 130  
 atgtttccta ttcgttttta acgtccggcg ttgctctgta tggcgatgct gacggttgtt 60  
 ctgagtggct gcgggctgat tcagaaagt gtggatgaat cgaaaagcgt ggcctcagcc 120  
 gttttctaca aacaaatcaa aatactgcat ctcgatttct tctcccgag cgcctgaat 180  
 acggatgogg aagatacgcc gctttccacg atggtgcatg tctggcaact gaaaaccgc 240  
 gaagattttg acaaggcgga ttacgacacc ctgtttatgc aggaagagaa gacgctggag 300  
 aaggacgtac tggcaaaaca caccgtctgg gtaaaaccgg aaggcacggc atccctgaat 360  
 gtgccgctgg ataaagagac gcagtttgtc gccattattg ggcagtttta tcacctgat 420  
 gaaaaaagcg acagctggcg tctggtgatc aaaaggacg aactggaggc cgacaagccg 480  
 cgctcgattg aactgatgag aagcgacctg cgactgctgc ctctcaagga taaa 534

<210> 131 <211> 627 <212> DNA <213> Escherichia coli <400> 131  
 atgttcttaa aaagaaaatg gtattacgca gtgacgacat ctgtcgcat tactttgtgt 60  
 ggtggaggat attatatgta caggcaagaa tatcagatgg ttgtcactgt accaactgct 120  
 gacgcgaacg atcccaactg gccaaataaa aggatacagt ttgataccag cgaatggcta 180  
 cagcaacttc aatataattaa aatagatgat cattatatat tgaatactca atatactcca 240  
 attgctaatt tggatgactt tggattaca ttaaaattac agaacgcatt aaatgggtcg 300  
 gataaaagac ttctgcact atatggcctt gctgagatgg atgctcagaa atttaaagac 360  
 ctgatgcgcg gtaaaattaa atgtgaatat ctgaggacga catttgatgc ggaaacatta 420



aagcctgtca atgattatatt ccttatttct tttacttata aagataaagt gtatgaattt 480  
 gagacagaaa gaaaaatata taaaacaagt gatgatgggt attttttgtg ggcatattgat 540  
 aatactgtcc acgaagcagg ctattggcat aacacagatc cggctgcgta ttcctataga 600  
 gattaccaga atggtaaggc tgtgaaa 627

<210> 132 <211> 1272 <212> DNA <213> Escherichia coli <400> 132  
 atggataattt ggcggggaca ttcgtttctg atgacaattt ccgctagggt cagacaatac 60  
 gttttctctc ttatgtcaat tttattgcag gaacgaaaaa tgaatatatt cactttatcc 120  
 aaagcaccgc tatacctggt aatttacta tttttaccca cgatggccat ggctatcgat 180  
 ccacctgaac gcgaactttc gcgatttgcc ctgaaaacga attaccttca gtcccctgat 240  
 gaaggcgtct atgaactggc gtttgataat gccagtaaaa aggtgtttgc agcagtcacc 300  
 gatcgtgtaa atcgtgaagc caataaaggc tatctgtatt cgtttaattc agattcgcgtg 360  
 aaagtcgaaa ataaatacac gatgccatac cgggcatttt cgctggcgat aaatcaggat 420  
 aaacatcagc tctatatcgg acacaccagc tcagcgtccc tgcgtatcag tatgtttgac 480  
 accccaaccg gcaaaactgg aagaaccagc gacagggttaa gttttaaagc ggcaaacgct 540  
 gcagattcgc gttttgagca ttttcgccat atgggtttaca gccaggattc cgataccctg 600  
 tttgtgagtt atagcaatat gctgaaaacg gccgagggca tgaagcctct gcataagctg 660  
 ttaatgctcg acgggacgac gcttgcccta aaaggcgagg ttaaggatgc ttacaaaggt 720  
 acagcgtatg gtctgacgat ggatgaaaaa acacagaaaa tctacgttgg cggaagagat 780  
 tacatcaacg aaattgatgc gaaaaatcag acgctgctgc gtaccatccc gttgaaagat 840  
 ccgagaccac aaatcacaag tgtgcagaat ctggcggttg actccgcttc tgaccgtgcc 900  
 tttgtggttg tattcgacca tgacgatcgt tccggtacaa aagatggact ctatatattt 960  
 gacttacgcg acggtaaaca gcttggctat gtgcacacag gagccggagc taacgcggtg 1020  
 aaatacaatc cgaaatataa cgaactgtat gtcaccaact tcaactagcg caccatcagc 1080  
 gtagtggatg ccaccaaata cagcatcacc cgtgaattta acatgccggt ctacccaaac 1140  
 cagatggtgt tgtcggacga tatggatacc ctttacattg gcatcaaaga aggctttaac 1200  
 cgcgattggg atcctgatgt gtttgtggaa ggagctaaaag aacgtattct gagcattgat 1260  
 ttgaaaaagt cg 1272

<210> 133 <211> 163 <212> PRT <213> Escherichia coli <400> 133  
 Met Ala Ile Pro Ala Tyr Leu Trp Leu Lys Asp Asp Gly Gly Ala Asp  
 1 5 10 15  
 Ile Lys Gly Ser Val Asp Val Gln Gly Arg Glu Gly Ser Ile Glu Val  
 20 25 30

Val Ala Leu Asp His Asp Val Tyr Ile Pro Thr Asp Asn Asn Thr Gly  
35 40 45

Lys Leu Thr Gly Thr Arg Thr His Lys Pro Phe Thr Phe Thr Lys Glu  
50 55 60

Ile Asp Ala Ser Ser Pro Tyr Leu Tyr Lys Ala Val Thr Thr Gly Gln  
65 70 75 80

Thr Leu Lys Thr Ala Glu Phe Lys Phe Tyr Arg Ile Asn Asp Ala Gly  
85 90 95

Gln Glu Val Glu Tyr Phe Asn Ile Thr Leu Asp Asn Val Lys Leu Val  
100 105 110

Arg Val Ala Pro Leu Met His Asp Ile Lys Asp Pro Ser Arg Glu Lys  
115 120 125

His Asn His Leu Glu Arg Ile Glu Phe Arg Tyr Glu Lys Ile Thr Trp  
130 135 140

Thr Tyr Lys Asp Gly Asn Ile Ile His Ser Asp Ser Trp Asn Glu Arg  
145 150 155 160

Pro Ser Ala

<210> 134 <211> 550 <212> PRT <213> Escherichia coli <400> 134

Val Arg Asn Thr Leu Lys Gln Ala Ile Val Leu Trp Gly Met Val Leu  
1 5 10 15

Leu Leu Val Leu Trp Ser Val Phe Ile Ser Pro Ser Gly Val Leu Arg  
20 25 30

Trp Ala Gly Ala Ala Ala Ile Val Leu Ala Val Ala Ala Leu Leu Ile  
35 40 45

Tyr Arg Arg Arg Gln Ala Trp Thr Glu Met Thr Gly Asp Ala Gly Leu  
50 55 60

Ser Ser Leu Pro Pro Glu Thr Tyr Arg Gln Pro Val Val Leu Val Cys  
65 70 75 80

Gly Gly Leu Ser Ala His Leu Ser Thr Asp Ser Pro Val Arg Gln Val  
85 90 95

Ser Glu Gly Leu Tyr Leu His Val Pro Asp Glu Glu Gln Leu Val Ala  
100 105 110

Gln Val Glu Arg Leu Leu Thr Leu Arg Pro Ala Trp Ala Ser Gln Leu  
 115 120 125

Ala Val Ala Tyr Thr Ile Met Pro Gly Ile His Arg Asp Val Ala Val  
 130 135 140

Leu Ala Gly Arg Leu Arg Arg Phe Ala His Ser Met Ala Thr Val Arg  
 145 150 160

Arg Arg Ala Gly Val Asn Val Pro Trp Leu Leu Trp Ser Gly Leu Ser  
 165 170 175

Gly Ser Pro Leu Pro Glu Arg Ala Ser Ser Pro Trp Phe Ile Cys Thr  
 180 185 190

Gly Gly Glu Val Gln Val Ala Thr Ser Thr Glu Thr Thr Met Pro Ala  
 195 200 205

Gln Trp Ile Ala Gln Ser Gly Val Gln Glu Arg Ser Gln Arg Leu Cys  
 210 215 220

Tyr Leu Leu Lys Ala Glu Ser Leu Met Gln Trp Leu Asn Leu Asn Val  
 225 230 235 240

Leu Thr Ala Leu Asn Gly Pro Glu Ala Lys Cys Pro Pro Leu Ala Met  
 245 250 255

Thr Val Gly Leu Val Pro Ser Leu Pro Ala Val Asp Asn Asn Leu Trp  
 260 265 270

Gln Leu Trp Ile Thr Ala Arg Thr Gly Leu Thr Pro Asp Ile Ala Asp  
 275 280 285

Thr Gly Thr Asp Asp Ala Leu Pro Phe Pro Asp Ala Leu Leu Arg Gln  
 290 295 300

Leu Pro Arg Gln Ser Gly Phe Thr Pro Leu Arg Arg Ala Cys Val Thr  
 305 310 315 320

Met Leu Gly Val Thr Thr Val Ala Gly Ile Ala Ala Leu Cys Leu Ser  
 325 330 335

Ala Thr Ala Asn Arg Gln Leu Leu Arg Gln Val Gly Asp Asp Leu His  
 340 345 350

Arg Phe Tyr Ala Val Pro Val Glu Glu Phe Ile Thr Lys Ala Arg His  
 355 360 365

Leu Ser Val Leu Lys Asp Asp Ala Thr Met Leu Asp Gly Tyr Tyr Arg  
 370 375 380

Glu Gly Glu Pro Leu Arg Leu Gly Leu Gly Leu Tyr Pro Gly Glu Arg  
385 390 395 400

Ile Arg Gln Pro Val Leu Arg Ala Ile Arg Asp Trp Arg Pro Pro Glu  
405 410 415

Gln Lys Met Glu Val Thr Ala Ser Leu Gln Val Gln Thr Val Arg Leu  
420 425 430

Asp Ser Met Ser Leu Phe Asp Val Gly Gln Ala Arg Leu Lys Asp Gly  
435 440 445

Ser Thr Lys Val Leu Val Asp Ala Leu Val Asn Ile Arg Ala Lys Pro  
450 455 460

Gly Trp Leu Ile Leu Val Ala Gly Tyr Thr Asp Ala Thr Gly Asp Glu  
465 470 475 480

Lys Ser Asn Gln Gln Leu Ser Leu Arg Arg Ala Glu Ala Val Arg Asn  
485 490 495

Trp Met Leu Gln Thr Ser Asp Ile Pro Ala Thr Cys Phe Ala Val Gln  
500 505 510

Gly Leu Gly Glu Ser Gln Pro Ala Ala Thr Asn Asp Thr Pro Gln Gly  
515 520 525

Arg Ala Val Asn Arg Arg Val Glu Ile Ser Leu Val Pro Arg Ser Asp  
530 535 540

Ala Cys Gln Asp Val Lys  
545 550

<210> 135 <211> 194 <212> PRT <213> Escherichia coli <400> 135

Met Ile Lys Ser Thr Phe Trp Arg Ala Leu Ala Leu Thr Ala Thr Leu  
1 5 10 15

Ile Leu Thr Gly Cys Ser His Ser Gln Pro Glu Gln Glu Gly Arg Pro  
20 25 30

Gln Ala Trp Leu Gln Pro Gly Thr Leu Ile Thr Leu Pro Ala Pro Gly  
35 40 45

Ile Ser Pro Ala Val Asn Ser Gln Gln Leu Leu Thr Gly Ser Phe Asn  
50 55 60

Gly Lys Thr Gln Ser Leu Leu Val Met Leu Asn Ala Glu Asp Gln Lys  
65 70 75 80

Ile Thr Leu Ala Gly Leu Ser Ser Val Gly Ile Arg Leu Phe Leu Val  
85 90 95

Thr Tyr Asp Ala Lys Gly Leu Arg Ala Glu Gln Ser Ile Val Val Pro  
100 105 110

Gln Leu Pro Pro Ala Ser Gln Val Leu Ala Asp Val Met Leu Ser His  
115 120 125

Trp Pro Ile Ser Ala Trp Gln Pro Gln Leu Pro Thr Gly Trp Thr Leu  
130 135 140

Arg Asp Asn Gly Asp Lys Arg Glu Leu Arg Asn Ala Ser Gly Lys Leu  
145 150 155 160

Val Thr Glu Ile Thr Tyr Leu Asn Arg Gln Gly Lys Arg Val Pro Ile  
165 170 175

Ser Ile Glu Gln His Val Phe Lys Tyr His Ile Thr Ile Gln Tyr Leu  
180 185 190

Gly Asp

<210> 136 <211> 129 <212> PRT <213> Escherichia coli <400> 136

Met Lys Arg Tyr Ile Lys Trp Phe Ala Ile Thr Ile Phe Ile Ser Met  
1 5 10 15

Leu Ser Ala Cys Val Arg Thr Ala Pro Val Gln Gln Ile Ser Thr Thr  
20 25 30

Val Ser Val Gly His Thr Gln Glu Gln Val Lys Asn Ala Ile Leu Lys  
35 40 45

Ala Gly Ala Gln Arg Lys Trp Ile Met Thr Gln Val Ser Pro Gly Val  
50 55 60

Ile Lys Ala Arg Tyr Gln Thr Arg Asn His Val Ala Glu Val Arg Ile  
65 70 75 80

Thr Tyr Thr Ala Thr Tyr Tyr Asn Ile Lys Tyr Asp Ser Ser Leu Asn  
85 90 95

Leu Gln Ala Ser Asp Gly Lys Ile His Lys Asn Tyr Asn Arg Trp Val  
100 105 110

Arg Asn Leu Asp Lys Asp Ile Gln Val Asn Leu Ser Thr Gly Ala Thr  
115 120 125

Leu

&lt;210&gt; 137 &lt;211&gt; 415 &lt;212&gt; PRT &lt;213&gt; Escherichia coli &lt;400&gt; 137

Met Lys Arg Lys His Leu Leu Leu Leu Leu Leu Phe Ser Phe Ser Thr  
 1 5 10 15

Asn Ser Ala Pro Leu Tyr Ser Leu Ile Arg Glu Ala Val Met His Asp  
 20 25 30

Pro Ile Val Met Glu Ala Arg Ala Glu Leu Thr Ser Ala Gln Ser Arg  
 35 40 45

Ile Glu Gln Ala Ser Ser Ala His Trp Pro Val Val Thr Ala Thr Gly  
 50 55 60

Ser Lys Leu Leu Ser Gln Ser His Arg Tyr Ser Tyr Asp Tyr Asp Thr  
 65 70 75 80

Glu Asp Ile Leu Pro Gly Ile Arg Gly Glu Val Asn Ile Phe Ala Ser  
 85 90 95

Gly Ala Ile Glu Ala Asp Val Arg Arg Ser Glu Ser Glu Ala Glu Tyr  
 100 105 110

Tyr His Tyr Lys Met Glu Glu Thr Lys Glu Glu Thr Ile His Ser Phe  
 115 120 125

Val Ser Leu Tyr Leu Asp Ala Leu Arg Glu Lys Gln Ser Ile Ala Val  
 130 135 140

Leu Glu Gln Ser Leu Ser Arg His Asn Ala Ile Leu Asn Asp Leu Asn  
 145 150 155 160

Thr Ile Ser Ile His Asp Thr Gly Arg Glu Ser Glu Leu Val Gln Ala  
 165 170 175

Glu Ala Arg Arg Leu Met Val Arg Gln Gln Ile Asn Ser Arg Ser Arg  
 180 185 190

Val Leu Lys Thr Thr Leu Gly Lys Leu Ser Thr Trp Thr Lys Asn Pro  
 195 200 205

Val Thr Glu Ala Asp Leu Glu Asn Pro Phe Ser Arg Met Thr Glu Ala  
 210 215 220

Lys Leu Leu Thr Asp Phe Thr Gln Ala Pro Gln Lys Gly Asn Pro Ser  
 225 230 235 240

Trp Leu Ala Ser Gln Ala Asp Val Glu Ser Lys Lys Ala Ala Leu Lys  
245 250 255

Ala Gln Glu Leu Ala Arg Tyr Pro Arg Val Asp Leu Thr Gly Ser Val  
260 265 270

Thr Arg Asp Asp Gln Gln Ile Gly Val Asn Leu Ser Trp Asp Leu Phe  
275 280 285

Asn Arg Asn Ala Ser Tyr Gly Val Thr Glu Lys Ala Ala Gln Ile Val  
290 295 300

Ala Ala Thr Gly Arg Leu Asp Ser Val Ala Arg Met Ile Asp Glu Thr  
305 310 315 320

Gly Arg Leu Ser Leu Ile Thr Val Arg Gln Ser Arg Gly Glu Met Glu  
325 330 335

Thr Leu Arg Arg Gln Glu Gln Ala Ser Ala Arg Val Val Asp Phe Tyr  
340 345 350

Arg Leu Gln Phe Gln Val Ala Arg Lys Thr Leu Ile Glu Leu Leu Asn  
355 360 365

Ala Glu Asn Glu Leu Tyr Ser Val Gly Leu Ser Arg Val Gln Thr Glu  
370 375 380

Asp Gln Met Leu His Gly Met Leu Asp Tyr Leu Tyr Ser Gln Gly Met  
385 390 395 400

Leu Leu Lys Trp Ser Gly Val Asn Leu Ser Gly Glu Glu Glu Lys  
405 410 415

<210> 138 <211> 201 <212> PRT <213> Escherichia coli <400> 138

Met Lys Phe Leu Pro Leu Leu Ala Leu Leu Ile Ser Pro Phe Val Ser  
1 5 10 15

Ala Leu Thr Leu Asp Asp Leu Gln Gln Arg Phe Thr Glu Gln Pro Val  
20 25 30

Ile Arg Ala His Phe Asp Gln Thr Arg Thr Ile Lys Asp Leu Pro Gln  
35 40 45

Pro Leu Arg Ser Gln Gly Gln Met Leu Ile Ala Arg Asp Gln Gly Leu  
50 55 60

Leu Trp Asp Gln Thr Ser Pro Phe Pro Met Gln Leu Leu Leu Asp Asp  
65 70 75 80

Lys Arg Met Val Gln Val Ile Asn Gly Gln Pro Pro Gln Ile Ile Thr  
85 90 95

Ala Glu Asn Asn Pro Gln Met Phe Gln Phe Asn His Leu Leu Arg Ala  
100 105 110

Leu Phe Gln Ala Asp Arg Lys Val Leu Glu Gln Asn Phe Arg Val Glu  
115 120 125

Phe Ala Asp Lys Gly Glu Gly Arg Trp Thr Leu Arg Leu Thr Pro Thr  
130 135 140

Thr Thr Pro Leu Asp Lys Ile Phe Asn Thr Ile Asp Leu Ala Gly Lys  
145 150 155 160

Thr Tyr Leu Glu Ser Ile Gln Leu Asn Asp Lys Gln Gly Asp Arg Thr  
165 170 175

Asp Ile Ala Leu Thr Gln His Gln Leu Thr Pro Ala Gln Leu Thr Asp  
180 185 190

Asp Glu His Gln Arg Phe Ala Ala Gln  
195 200

<210> 139 <211> 770 <212> PRT <213> Escherichia coli <400> 139

Met Glu Asn Phe Phe Met Lys Asn Ser Lys Val Phe Tyr Arg Ser Ala  
1 5 10 15

Leu Ala Thr Ala Ile Val Met Ala Leu Ser Ala Pro Ala Phe Ala Thr  
20 25 30

Asp Ser Thr Val Ser Thr Asp Pro Val Thr Leu Asn Thr Glu Lys Thr  
35 40 45

Thr Leu Asp Gln Asp Val Val Ile Asn Gly Asp Asn Lys Ile Thr Ala  
50 55 60

Val Thr Ile Glu Thr Ser Asp Ser Asp Lys Asp Leu Asn Val Thr Phe  
65 70 75 80

Gly Gly His Asp Ile Thr Ala Ala Ser Thr Val Asn Gln Asp Phe Val  
85 90 95

Glu Gly Val Lys Val Ser Gly Asn Lys Asn Val Val Ile Asn Ala Thr  
100 105 110

Asp Ser Thr Ile Thr Ala Gln Gly Glu Gly Thr Tyr Val Arg Thr Ala  
115 120 125



Met Val Ile Asp Ser Thr Gly Asp Val Val Val Asn Gly Gly Asn Phe  
 130 135 140

Val Ala Lys Asn Glu Lys Gly Ser Ala Thr Gly Ile Ser Leu Glu Ala  
 145 150 155 160

Thr Thr Gly Asn Asn Leu Thr Leu Asn Gly Thr Thr Ile Asn Ala Gln  
 165 170 175

Gly Asn Lys Ser Tyr Ser Asn Gly Ser Thr Ala Ile Phe Ala Gln Lys  
 180 185 190

Gly Asn Leu Leu Gln Gly Phe Asp Gly Asp Ala Thr Asp Asn Ile Thr  
 195 200 205

Leu Ala Asp Ser Asn Ile Ile Asn Gly Gly Ile Glu Thr Ile Val Thr  
 210 215 220

Ala Gly Asn Lys Thr Gly Ile His Thr Val Asn Leu Asn Ile Lys Asp  
 225 230 235 240

Gly Ser Val Ile Gly Ala Ala Asn Asn Lys Gln Thr Ile Tyr Ala Ser  
 245 250 255

Ala Ser Ala Gln Gly Ala Gly Ser Ala Thr Gln Asn Leu Asn Leu Ser  
 260 265 270

Val Ala Asp Ser Thr Ile Tyr Ser Asp Val Leu Ala Leu Ser Glu Ser  
 275 280 285

Glu Asn Ser Ala Ser Thr Thr Thr Asn Val Asn Met Asn Val Ala Arg  
 290 295 300

Ser Tyr Trp Glu Gly Asn Ala Tyr Thr Phe Asn Ser Gly Asp Lys Ala  
 305 310 315 320

Gly Ser Asp Leu Asp Ile Asn Leu Ser Asp Ser Ser Val Trp Lys Gly  
 325 330 335

Lys Val Ser Gly Ala Gly Asp Ala Ser Val Ser Leu Gln Asn Gly Ser  
 340 345 350

Val Trp Asn Val Thr Gly Ser Ser Thr Val Asp Ala Leu Ala Val Lys  
 355 360 365

Asp Ser Thr Val Asn Ile Thr Lys Ala Thr Val Asn Thr Gly Thr Phe  
 370 375 380

Ala Ser Gln Asn Gly Thr Leu Ile Val Asp Ala Ser Ser Glu Asn Thr  
 385 390 395 400  
 Leu Asp Ile Ser Gly Lys Ala Ser Gly Asp Leu Arg Val Tyr Ser Ala  
 405 410 415  
 Gly Ser Leu Asp Leu Ile Asn Glu Gln Thr Ala Phe Ile Ser Thr Gly  
 420 425 430  
 Lys Asp Ser Thr Leu Lys Ala Thr Gly Thr Thr Glu Gly Gly Leu Tyr  
 435 440 445  
 Gln Tyr Asp Leu Thr Gln Gly Ala Asp Gly Asn Phe Tyr Phe Val Lys  
 450 455 460  
 Asn Thr His Lys Ala Ser Asn Ala Ser Ser Val Ile Gln Ala Met Ala  
 465 470 475 480  
 Ala Ala Pro Ala Asn Val Ala Asn Leu Gln Ala Asp Thr Leu Ser Ala  
 485 490 495  
 Arg Gln Asp Ala Val Arg Leu Ser Glu Asn Asp Lys Gly Gly Val Trp  
 500 505 510  
 Ile Gln Tyr Phe Gly Gly Lys Gln Lys His Thr Thr Ala Gly Asn Ala  
 515 520 525  
 Ser Tyr Asp Leu Asp Val Asn Gly Val Met Leu Gly Gly Asp Thr Arg  
 530 535 540  
 Phe Met Thr Glu Asp Gly Ser Trp Leu Ala Gly Val Ala Met Ser Ser  
 545 550 555 560  
 Ala Lys Gly Asp Met Thr Thr Met Gln Ser Lys Gly Asp Thr Glu Gly  
 565 570 575  
 Tyr Ser Phe His Ala Tyr Leu Ser Arg Gln Tyr Asn Asn Gly Ile Phe  
 580 585 590  
 Ile Asp Thr Ala Ala Gln Phe Gly His Tyr Ser Asn Thr Ala Asp Val  
 595 600 605  
 Arg Leu Met Asn Gly Gly Gly Thr Ile Lys Ala Asp Phe Asn Thr Asn  
 610 615 620  
 Gly Phe Gly Ala Met Val Lys Gly Gly Tyr Thr Trp Lys Asp Gly Asn  
 625 630 635 640  
 Gly Leu Phe Ile Gln Pro Tyr Ala Lys Leu Ser Ala Leu Thr Leu Glu  
 645 650 655

Gly Val Asp Tyr Gln Leu Asn Gly Val Asp Val His Ser Asp Ser Tyr  
660 665 670

Asn Ser Val Leu Gly Glu Ala Gly Thr Arg Val Gly Tyr Asp Phe Ala  
675 680 685

Val Gly Asn Ala Thr Val Lys Pro Tyr Leu Asn Leu Ala Ala Leu Asn  
690 695 700

Glu Phe Ser Asp Gly Asn Lys Val Arg Leu Gly Asp Glu Ser Val Asn  
705 710 715 720

Ala Ser Ile Asp Gly Ala Ala Phe Arg Val Gly Ala Gly Val Gln Ala  
725 730 735

Asp Ile Thr Lys Asn Met Gly Ala Tyr Ala Ser Leu Asp Tyr Thr Lys  
740 745 750

Gly Asp Asp Ile Glu Asn Pro Leu Gln Gly Val Val Gly Ile Asn Val  
755 760 765

Thr Trp  
770

<210> 140 <211> 660 <212> PRT <213> Escherichia coli <400> 140

Met Ser Arg Pro Gln Phe Thr Ser Leu Arg Leu Ser Leu Leu Ala Leu  
1 5 10 15

Ala Val Ser Ala Thr Leu Pro Thr Phe Ala Phe Ala Thr Glu Thr Met  
20 25 30

Thr Val Thr Ala Thr Gly Asn Ala Arg Ser Ser Phe Glu Ala Pro Met  
35 40 45

Met Val Ser Val Ile Asp Thr Ser Ala Pro Glu Asn Gln Thr Ala Thr  
50 55 60

Ser Ala Thr Asp Leu Leu Arg His Val Pro Gly Ile Thr Leu Asp Gly  
65 70 75 80

Thr Gly Arg Thr Asn Gly Gln Asp Val Asn Met Arg Gly Tyr Asp His  
85 90 95

Arg Gly Val Leu Val Leu Val Asp Gly Val Arg Gln Gly Thr Asp Thr  
100 105 110

Gly His Leu Asn Gly Thr Phe Leu Asp Pro Ala Leu Ile Lys Arg Val  
115 120 125

Glu Ile Val Arg Gly Pro Ser Ala Leu Leu Tyr Gly Ser Gly Ala Leu  
 130 135 140

Gly Gly Val Ile Ser Tyr Asp Thr Val Asp Ala Lys Asp Leu Leu Gln  
 145 150 155 160

Glu Gly Gln Ser Ser Gly Phe Arg Val Phe Gly Thr Gly Gly Thr Gly  
 165 170 175

Asp His Ser Leu Gly Leu Gly Ala Ser Ala Phe Gly Arg Thr Glu Asn  
 180 185 190

Leu Asp Gly Ile Val Ala Trp Ser Ser Arg Asp Arg Gly Asp Leu Arg  
 195 200 205

Gln Ser Asn Gly Glu Thr Ala Pro Asn Asp Glu Ser Ile Asn Asn Met  
 210 215 220

Leu Ala Lys Gly Thr Trp Gln Ile Asp Ser Ala Gln Ser Leu Ser Gly  
 225 230 235 240

Leu Val Arg Tyr Tyr Asn Asn Asp Ala Arg Glu Pro Lys Asn Pro Gln  
 245 250 255

Thr Val Glu Ala Ser Asp Ser Ser Asn Pro Met Val Asp Arg Ser Thr  
 260 265 270

Ile Gln Arg Asp Ala Gln Leu Ser Tyr Lys Leu Ala Pro Gln Gly Asn  
 275 280 285

Asp Trp Leu Asn Ala Asp Ala Lys Ile Tyr Trp Ser Glu Val Arg Ile  
 290 295 300

Asn Ala Gln Asn Thr Gly Ser Ser Gly Glu Tyr Arg Glu Gln Ile Thr  
 305 310 315 320

Lys Gly Ala Arg Leu Glu Asn Arg Ser Thr Leu Phe Ala Asp Ser Phe  
 325 330 335

Ala Ser His Leu Leu Thr Tyr Gly Gly Glu Tyr Tyr Arg Gln Glu Gln  
 340 345 350

His Pro Gly Gly Ala Thr Thr Gly Phe Pro Gln Ala Lys Ile Asp Phe  
 355 360 365

Ser Ser Gly Trp Leu Gln Asp Glu Ile Thr Leu Arg Asp Leu Pro Ile  
 370 375 380

Thr Leu Leu Gly Gly Thr Arg Tyr Asp Ser Tyr Arg Gly Ser Ser Asp  
 385 390 395 400

Gly Tyr Lys Asp Val Asp Ala Asp Lys Trp Ser Ser Arg Ala Gly Met  
 405 410 415

Thr Ile Asn Pro Thr Asn Trp Leu Met Leu Phe Gly Ser Tyr Ala Gln  
 420 425 430

Ala Phe Arg Ala Pro Thr Met Gly Glu Met Tyr Asn Asp Ser Lys His  
 435 440 445

Phe Ser Ile Gly Arg Phe Tyr Thr Asn Tyr Trp Val Pro Asn Pro Asn  
 450 455 460

Leu Arg Pro Glu Thr Asn Glu Thr Gln Glu Tyr Gly Phe Gly Leu Arg  
 465 470 475 480

Phe Asp Asp Leu Met Leu Ser Asn Asp Ala Leu Glu Phe Lys Ala Ser  
 485 490 495

Tyr Phe Asp Thr Lys Ala Lys Asp Tyr Ile Ser Thr Thr Val Asp Phe  
 500 505 510

Ala Ala Ala Thr Thr Met Ser Tyr Asn Val Pro Asn Ala Lys Ile Trp  
 515 520 525

Gly Trp Asp Val Met Thr Lys Tyr Thr Thr Asp Leu Phe Ser Leu Asp  
 530 535 540

Val Ala Tyr Asn Arg Thr Arg Gly Lys Asp Thr Asp Thr Gly Glu Tyr  
 545 550 555 560

Ile Ser Ser Ile Asn Pro Asp Thr Val Thr Ser Thr Leu Asn Ile Pro  
 565 570 575

Ile Ala His Ser Gly Phe Ser Val Gly Trp Val Gly Thr Phe Ala Asp  
 580 585 590

Arg Ser Thr His Ile Ser Ser Ser Tyr Ser Lys Gln Pro Gly Tyr Gly  
 595 600 605

Val Asn Asp Phe Tyr Val Ser Tyr Gln Gly Gln Gln Ala Leu Lys Gly  
 610 615 620

Met Thr Thr Thr Leu Val Leu Gly Asn Ala Phe Asp Lys Glu Tyr Trp  
 625 630 635 640

Ser Pro Gln Gly Ile Pro Gln Asp Gly Arg Asn Gly Lys Ile Phe Val  
 645 650 655

Ser Tyr Gln Trp  
660

<210> 141 <211> 719 <212> PRT <213> Escherichia coli <400> 141

Met Arg Asp Glu Met Leu Tyr Asn Ile Pro Cys Arg Ile Tyr Ile Leu  
1 5 10 15

Ser Thr Leu Ser Leu Cys Ile Ser Gly Ile Val Ser Thr Ala Thr Ala  
20 25 30

Thr Ser Ser Glu Thr Lys Ile Ser Asn Glu Glu Thr Leu Val Val Thr  
35 40 45

Thr Asn Arg Ser Ala Ser Asn Leu Trp Glu Ser Pro Ala Thr Ile Gln  
50 55 60

Val Ile Asp Gln Gln Thr Leu Gln Asn Ser Thr Asn Ala Ser Ile Ala  
65 70 75 80

Asp Asn Leu Gln Asp Ile Pro Gly Val Glu Ile Thr Asp Asn Ser Leu  
85 90 95

Ala Gly Arg Lys Gln Ile Arg Ile Arg Gly Glu Ala Ser Ser Arg Val  
100 105 110

Leu Ile Leu Ile Asp Gly Gln Glu Val Thr Tyr Gln Arg Ala Gly Asp  
115 120 125

Asn Tyr Gly Val Gly Leu Leu Ile Asp Glu Ser Ala Leu Glu Arg Val  
130 135 140

Glu Val Val Lys Gly Pro Tyr Ser Val Leu Tyr Gly Ser Gln Ala Ile  
145 150 155 160

Gly Gly Ile Val Asn Phe Ile Thr Lys Lys Gly Gly Asp Lys Leu Ala  
165 170 175

Ser Gly Val Val Lys Ala Val Tyr Asn Ser Ala Thr Ala Gly Trp Glu  
180 185 190

Glu Ser Ile Ala Val Gln Gly Ser Ile Gly Gly Phe Asp Tyr Arg Ile  
195 200 205

Asn Gly Ser Tyr Ser Asp Gln Gly Asn Arg Asp Thr Pro Asp Gly Arg  
210 215 220

Leu Pro Asn Thr Asn Tyr Arg Asn Asn Ser Gln Gly Val Trp Leu Gly  
225 230 235 240

Leu Arg Ala Ala Phe Ala Gln Gly Tyr Val Phe Pro Thr Leu Ser Gln  
485 490 495

Leu Phe Met Gln Thr Ser Ala Gly Gly Ser Val Thr Tyr Gly Asn Pro  
 500 505 510  
 Asp Leu Lys Ala Glu His Ser Asn Asn Phe Glu Leu Gly Ala Arg Tyr  
 515 520 525  
 Asn Gly Asn Thr Trp Leu Ile Asp Ser Ala Val Tyr Tyr Ser Glu Ala  
 530 535 540  
 Lys Asp Tyr Ile Ala Ser Leu Ile Cys Asp Gly Ser Ile Val Cys Asn  
 545 550 555 560  
 Gly Asn Thr Asn Ser Ser Arg Ser Ser Tyr Tyr Tyr Tyr Asp Asn Ile  
 565 570 575  
 Asp Arg Ala Lys Thr Trp Gly Leu Glu Ile Ser Ala Glu Tyr Asn Gly  
 580 585 590  
 Trp Val Phe Ser Pro Tyr Ile Ser Gly Asn Leu Ile Arg Arg Gln Tyr  
 595 600 605  
 Glu Thr Ser Thr Leu Lys Thr Thr Asn Thr Gly Glu Pro Ala Ile Asn  
 610 615 620  
 Gly Arg Ile Gly Leu Lys His Thr Leu Val Met Gly Gln Ala Asn Ile  
 625 630 635 640  
 Ile Ser Asp Val Phe Ile Arg Ala Ala Ser Ser Ala Lys Asp Asp Ser  
 645 650 655  
 Asn Gly Thr Glu Thr Asn Val Pro Gly Trp Ala Thr Leu Asn Phe Ala  
 660 665 670  
 Val Asn Thr Glu Phe Gly Asn Glu Asp Gln Ser Arg Ile Asn Leu Ala  
 675 680 685  
 Leu Asn Asn Leu Thr Asp Lys Arg Tyr Arg Thr Ala His Glu Thr Ile  
 690 695 700  
 Pro Ala Ala Gly Phe Asn Ala Ala Ile Gly Phe Val Trp Asn Phe  
 705 710 715  
 <210> 142 <211> 199 <212> PRT <213> Escherichia coli <400> 142  
 Met Arg Lys Val Cys Ala Val Ile Leu Ser Ala Ala Ile Cys Leu Ser  
 1 5 10 15  
 Val Ser Gly Ala Pro Ala Trp Ala Ser Glu His Gln Ser Thr Leu Ser  
 20 25 30



Ala Gly Tyr Leu His Ala Arg Thr Asn Ala Pro Gly Ser Asp Asn Leu  
35 40 45

Asn Gly Ile Asn Val Lys Tyr Arg Tyr Glu Phe Thr Asp Ala Leu Gly  
50 55 60

Leu Ile Thr Ser Phe Ser Tyr Ala Asn Ala Glu Asp Glu Gln Lys Thr  
65 70 75 80

His Tyr Ser Asp Thr Arg Trp His Glu Asp Ser Val Arg Asn Arg Trp  
85 90 95

Phe Ser Val Met Ala Gly Pro Ser Val Arg Val Asn Glu Trp Phe Ser  
100 105 110

Ala Tyr Ser Met Ala Gly Val Ala Tyr Ser Arg Val Ser Thr Phe Ser  
115 120 125

Gly Asp Tyr Leu Arg Val Thr Asp Asn Lys Gly Lys Thr His Asp Val  
130 135 140

Leu Thr Gly Ser Asp Asp Gly Arg His Ser Asn Thr Ser Leu Ala Trp  
145 150 155 160

Gly Ala Gly Val Gln Phe Asn Pro Thr Glu Ser Val Thr Ile Asp Leu  
165 170 175

Ala Tyr Glu Gly Ser Gly Ser Gly Asp Trp Arg Thr Asp Ala Phe Ile  
180 185 190

Val Gly Ile Gly Tyr Arg Phe  
195

<210> 143 <211> 456 <212> PRT <213> Escherichia coli <400> 143

Met Lys Lys Ser Thr Leu Ser Leu Ala Ile Gly Leu Leu Leu Ala Cys  
1 5 10 15

Ser Thr Gly Met Ala Lys Thr Gln His Leu Thr Leu Glu Gln Arg Leu  
20 25 30

Glu Ala Ala Glu Met Arg Ala Ala Lys Ala Glu Gly Gln Val Lys Gln  
35 40 45

Leu Gln Thr Gln Gln Ala Ala Glu Ile Arg Glu Ile Lys Thr Ala Gln  
50 55 60

Gly Asn Thr Pro Val Asn Gly Gln Ser Thr Thr Glu Ser Glu Lys Lys  
65 70 75 80

Asn	Ala	Thr	Pro	Pro	Asn	Leu	Leu	Leu	Ser	Gly	Tyr	Gly	Asp	Leu	Lys
				85					90					95	
Ile	Tyr	Gly	Asp	Val	Glu	Phe	Asn	Met	Asp	Ala	Glu	Ser	Asn	His	Gly
			100					105					110		
Leu	Leu	Ala	Met	Thr	Asn	Ala	Asp	Val	Asn	Ser	Asp	Pro	Thr	Asn	Glu
		115					120					125			
Trp	Asn	Leu	Asn	Gly	Arg	Ile	Leu	Leu	Gly	Phe	Asp	Gly	Met	Arg	Lys
	130					135					140				
Leu	Asp	Asn	Gly	Tyr	Phe	Ala	Gly	Phe	Ser	Ala	Gln	Pro	Leu	Gly	Asp
145					150					155					160
Met	His	Gly	Ser	Val	Asn	Ile	Asp	Asp	Ala	Val	Phe	Phe	Phe	Gly	Lys
				165					170					175	
Glu	Asn	Asp	Trp	Lys	Val	Lys	Val	Gly	Arg	Phe	Glu	Ala	Tyr	Asp	Met
			180					185					190		
Phe	Pro	Leu	Asn	Gln	Asp	Thr	Phe	Val	Glu	His	Ser	Gly	Asn	Thr	Ala
		195					200					205			
Asn	Asp	Leu	Tyr	Asp	Asp	Gly	Ser	Gly	Tyr	Ile	Tyr	Met	Met	Lys	Glu
	210					215					220				
Gly	Arg	Gly	Arg	Ser	Asn	Ala	Gly	Gly	Asn	Phe	Leu	Val	Ser	Lys	Gln
225					230					235					240
Leu	Asp	Asn	Trp	Tyr	Phe	Glu	Leu	Asn	Thr	Leu	Leu	Glu	Asp	Gly	Thr
				245					250					255	
Ser	Leu	Tyr	Asn	Asp	Gly	Asn	Tyr	His	Gly	Arg	Asp	Met	Glu	Gln	Gln
			260					265					270		
Lys	Asn	Val	Ala	Tyr	Leu	Arg	Pro	Val	Ile	Ala	Trp	Ser	Pro	Thr	Glu
		275					280					285			
Glu	Phe	Thr	Val	Ser	Ala	Ala	Met	Glu	Ala	Asn	Val	Val	Asn	Asn	Ala
	290					295					300				
Tyr	Gly	Tyr	Thr	Asp	Ser	Lys	Gly	Asn	Phe	Val	Asp	Gln	Ser	Asp	Arg
305					310					315					320
Thr	Gly	Tyr	Gly	Met	Ser	Met	Thr	Trp	Asn	Gly	Leu	Lys	Thr	Asp	Pro
				325					330					335	
Glu	Asn	Gly	Ile	Val	Val	Asn	Leu	Asn	Thr	Ala	Tyr	Leu	Asp	Ala	Asn
			340					345					350		

Asn Glu Lys Asp Phe Thr Ala Gly Ile Asn Ala Leu Trp Lys Arg Phe  
 355 360 365

Glu Leu Gly Tyr Ile Tyr Ala His Asn Lys Ile Asp Glu Phe Ser Gly  
 370 375 380

Val Val Cys Asp Asn Asp Cys Trp Ile Asp Asp Glu Gly Thr Tyr Asn  
 385 390 395 400

Ile His Thr Ile His Ala Ser Tyr Gln Phe Ala Asn Val Met Asp Met  
 405 410 415

Glu Asn Phe Asn Ile Tyr Leu Gly Thr Tyr Tyr Ser Ile Leu Asp Ser  
 420 425 430

Asp Gly Asp Lys Ile His Gly Asp Asp Ser Asp Asp Arg Tyr Gly Ala  
 435 440 445

Arg Val Arg Phe Lys Tyr Phe Phe  
 450 455

<210> 144 <211> 174 <212> PRT <213> Escherichia coli <400> 144

Met Asn Gly Lys Ala Phe Leu Ala Cys Val Leu Met Ser Val Val Leu  
 1 5 10 15

Thr Gly Cys Glu Thr Ala Lys Lys Ile Ser Gln Val Ile Arg Asn Pro  
 20 25 30

Asp Ile Gln Val Gly Lys Leu Met Asp Gln Ser Thr Glu Leu Thr Val  
 35 40 45

Thr Leu Leu Thr Glu Pro Asp Ser Asn Leu Thr Ala Asp Gly Glu Ala  
 50 55 60

Ala Pro Val Asp Val Gln Leu Val Tyr Leu Ser Asp Asp Ser Lys Phe  
 65 70 75 80

His Ala Ala Asp Tyr Asp Gln Val Ala Thr Thr Ala Leu Pro Asp Val  
 85 90 95

Leu Gly Lys Asn Tyr Ile Asp His Gln Asp Phe Asn Leu Leu Pro Asp  
 100 105 110

Thr Val Lys Thr Leu Pro Pro Ile Lys Leu Asp Glu Lys Thr Gly Tyr  
 115 120 125

Ile Gly Val Ile Ala Tyr Phe Ser Asp Asp Gln Ala Thr Glu Trp Lys  
 130 135 140

Gln Ile Glu Ser Val Glu Ser Ile Gly His His Tyr Arg Leu Leu Val  
 145 150 155 160

His Ile Arg Ala Ser Ala Ile Glu Met Lys Lys Glu Glu Asn  
 165 170

<210> 145 <211> 1144 <212> PRT <213> Escherichia coli <400> 145

Leu Thr Leu Ala Trp Ile Phe Leu Leu Val Trp Ile Trp Trp Gln Gly  
 1 5 10 15

Pro Lys Trp Thr Leu Tyr Glu Gln His Trp Leu Ala Pro Leu Ala Asn  
 20 25 30

Arg Trp Leu Ala Thr Ala Val Trp Gly Leu Ile Ala Leu Val Trp Leu  
 35 40 45

Thr Trp Arg Val Met Lys Arg Leu Gln Lys Leu Glu Lys Gln Gln Lys  
 50 55 60

Gln Gln Arg Glu Glu Glu Lys Asp Pro Leu Thr Val Glu Leu His Arg  
 65 70 75 80

Gln Gln Gln Tyr Leu Asp His Trp Leu Leu Arg Leu Arg Arg His Leu  
 85 90 95

Asp Asn Arg Arg Tyr Leu Trp Gln Leu Pro Trp Tyr Met Val Ile Gly  
 100 105 110

Pro Ala Gly Ser Gly Lys Ser Thr Leu Leu Arg Glu Gly Phe Pro Ser  
 115 120 125

Asp Ile Val Tyr Thr Pro Glu Ser Ile Arg Gly Val Glu Tyr His Pro  
 130 135 140

Leu Ile Thr Pro Arg Val Gly Asn Gln Ala Val Ile Phe Asp Val Asp  
 145 150 155 160

Gly Val Leu Thr Thr Pro Gly Gly Asp Asp Leu Leu Arg Arg Arg Leu  
 165 170 175

Arg Glu His Trp Leu Gly Trp Leu Met Gln Thr Arg Ala Arg Gln Pro  
 180 185 190

Leu Asn Gly Leu Ile Leu Thr Leu Asp Leu Pro Asp Leu Leu Thr Ala  
 195 200 205

Asp Lys Ser Arg Arg Glu Thr Leu Val Gln Asn Leu Arg Gln Gln Leu  
 210 215 220

Gln Glu Ile Arg Gln Ser Leu His Cys Arg Leu Pro Val Tyr Val Val  
 225 230 235 240

Leu Thr Arg Leu Asp Leu Leu Asn Gly Phe Ala Ala Leu Phe His Ser  
 245 250 255

Leu Asp Lys Lys Asp Arg Asp Ala Ile Leu Gly Val Thr Phe Thr Arg  
 260 265 270

Arg Ala His Glu Ser Asp Gly Trp Arg Ser Glu Leu Gly Ala Phe Trp  
 275 280 285

Gln Thr Trp Val Gln Gln Val Asn Leu Ala Leu Ser Asp Leu Val Leu  
 290 295 300

Ala Gln Thr Gly Ala Ala Pro Arg Ser Ala Val Phe Ser Phe Ser Arg  
 305 310 315 320

Gln Met Gln Gly Thr Gly Glu Ile Val Thr Ala Leu Leu Ala Ala Leu  
 325 330 335

Leu Asp Gly Glu Asn Met Asp Val Met Leu Arg Gly Val Trp Leu Thr  
 340 345 350

Ser Ser Leu Gln Arg Gly Gln Val Asp Asp Ile Phe Thr Gln Ser Ala  
 355 360 365

Ala Arg Gln Tyr Gly Leu Gly Asn Ser Ser Leu Ala Thr Trp Pro Leu  
 370 375 380

Val Glu Thr Thr Pro Tyr Phe Thr Arg Arg Leu Phe Pro Glu Val Leu  
 385 390 395 400

Leu Ala Glu Pro Asn Leu Ala Gly Glu Asn Ser Val Trp Leu Asn Ser  
 405 410 415

Ser Arg Arg Arg Leu Thr Ala Phe Ser Thr Cys Gly Ala Ala Leu Ala  
 420 425 430

Ala Leu Met Val Gly Ser Trp His His Tyr Tyr Asn Gln Asn Trp Gln  
 435 440 445

Ser Gly Val Asn Val Leu Ala Gln Ala Lys Ala Phe Met Asp Val Pro  
 450 455 460

Pro Pro Gln Gly Thr Asp Glu Phe Gly Asn Leu Gln Leu Pro Leu Leu  
 465 470 475 480

Asn Pro Val Arg Asp Ala Thr Leu Ala Tyr Gly Asp Tyr Arg Asp His  
 485 490 495

Gly Phe Leu Ala Asp Met Gly Leu Tyr Gln Gly Ala Arg Val Gly Pro  
 500 505 510

Tyr Val Glu Gln Thr Tyr Ile Gln Leu Leu Glu Gln Arg Tyr Leu Pro  
 515 520 525

Ser Leu Met Asn Gly Leu Ile Arg Asp Leu Asn Ile Ala Pro Pro Glu  
 530 535 540

Ser Glu Glu Lys Leu Ala Val Leu Arg Val Val Arg Met Met Glu Asp  
 545 550 555 560

Lys Ser Gly Arg Asn Asn Glu Ala Val Lys Gln Tyr Met Ala Arg Arg  
 565 570 575

Trp Ser Asn Glu Phe His Gly Gln Arg Asp Ile Gln Ala Gln Leu Met  
 580 585 590

Val His Leu Asp Tyr Ala Leu Glu His Thr Asp Trp His Ala Gln Arg  
 595 600 605

Gln Ser Ser Asp Ser Asp Ala Val Ser Arg Trp Thr Pro Tyr Asp Lys  
 610 615 620

Pro Ile Ile Asn Ala Gln Gln Glu Leu Ser Lys Leu Pro Ile Tyr Gln  
 625 630 635 640

Arg Val Tyr Gln Thr Leu Arg Thr Lys Ala Leu Ser Val Leu Pro Ala  
 645 650 655

Asp Leu Asn Leu Arg Asp Gln Val Gly Pro Thr Phe Asp Asn Val Phe  
 660 665 670

Val Ala Gly Asn Asp Glu Lys Leu Val Ile Pro Gln Phe Leu Thr Arg  
 675 680 685

Tyr Gly Leu Gln Ser Tyr Phe Val Lys Gln Arg Glu Gly Leu Val Glu  
 690 695 700

Leu Thr Ala Leu Asp Ser Trp Val Leu Asn Leu Thr Gln Ser Val Ala  
 705 710 715 720

Tyr Ser Glu Ala Asp Arg Glu Glu Ile Gln Arg His Ile Thr Glu Gln  
 725 730 735

Tyr Ile Ser Asp Tyr Thr Ala Thr Trp Arg Ala Gly Met Asp Asn Leu  
 740 745 750

Asn Val Arg Asp Tyr Glu Ala Met Ser Ala Leu Thr Asp Ala Leu Glu  
755 760 765

Gln Ile Ile Ser Gly Asp Gln Pro Phe Gln Arg Ala Leu Thr Ala Leu  
770 775 780

Arg Asp Asn Thr His Ala Leu Thr Leu Ser Gly Lys Leu Asp Asp Lys  
785 790 795 800

Ala Arg Glu Ala Ala Ile Asn Glu Met Asp Tyr Arg Leu Leu Ser Arg  
805 810 815

Leu Gly His Glu Phe Ala Pro Glu Asn Ser Ala Leu Glu Glu Gln Lys  
820 825 830

Asp Lys Ala Ser Thr Leu Gln Ala Val Tyr Gln Gln Leu Thr Glu Leu  
835 840 845

His Arg Tyr Leu Leu Ala Ile Gln Asn Ser Pro Val Pro Gly Lys Ser  
850 855 860

Ala Leu Lys Ala Val Gln Leu Arg Leu Asp Gln Asn Ser Ser Asp Pro  
865 870 875 880

Ile Phe Ala Thr Arg Gln Met Ala Lys Thr Leu Pro Ala Pro Leu Asn  
885 890 895

Arg Trp Val Gly Lys Leu Ala Asp Gln Ala Trp His Val Val Met Val  
900 905 910

Glu Ala Val Arg Tyr Met Glu Val Asp Trp Arg Asp Asn Val Val Lys  
915 920 925

Pro Phe Asn Glu Gln Leu Ala Asp Asn Tyr Pro Phe Asn Pro Arg Ala  
930 935 940

Thr Gln Asp Ala Ser Leu Asp Ser Phe Glu Arg Phe Phe Lys Pro Asp  
945 950 955 960

Gly Ile Leu Asp Asn Phe Tyr Lys Asn Asn Leu Arg Leu Phe Leu Glu  
965 970 975

Asn Asp Leu Thr Phe Gly Asp Asp Gly Arg Val Leu Ile Arg Glu Asp  
980 985 990

Ile Arg Gln Gln Leu Asp Thr Ala Gln Lys Ile Arg Asp Ile Phe Phe  
995 1000 1005

Ser Gln Gln Asn Gly Leu Gly Ala Gln Phe Ala Val Glu Thr Val  
1010 1015 1020

Ser Leu Ser Gly Asn Lys Arg Arg Ser Val Leu Asn Leu Asp Gly  
1025 1030 1035

Gln Leu Val Asp Tyr Ser Gln Gly Arg Asn Tyr Thr Ala His Leu  
1040 1045 1050

Val Trp Pro Asn Asn Met Arg Glu Gly Asn Glu Ser Lys Leu Thr  
1055 1060 1065

Leu Ile Gly Thr Ser Gly Arg Ala Pro Arg Ser Ile Ala Phe Ser  
1070 1075 1080

Gly Pro Trp Ala Gln Phe Arg Leu Phe Gly Ala Gly Gln Leu Thr  
1085 1090 1095

Asn Val Thr Ser Asp Thr Phe Asn Val Arg Phe Asn Val Asp Gly  
1100 1105 1110

Gly Ala Met Val Tyr Gln Val His Val Asp Thr Glu Asp Asn Pro  
1115 1120 1125

Phe Thr Gly Gly Leu Phe Ser Leu Phe Arg Leu Pro Asp Thr Leu  
1130 1135 1140

Tyr

<210> 146 <211> 489 <212> DNA <213> Escherichia coli <400> 146  
atggctattc ctgcttatct ctggctgaaa gatgacggcg gcgcggatat caaaggttcc 60  
gtggacgttc aggggcgcga aggtagcatc gaagtgggtg cgctggatca cgatgtgtac 120  
atcccgaccg acaataacac cggcaaactg accggtaccc gtactcacia gccttttacg 180  
tttaccaaag aaatcgatgc gtccagcccg tatctctaca aagctgtgac caccggacag 240  
accctgaaaa cggcagaatt taagttttac cgcataacg atgccggtca ggaagtggag 300  
tacttcaaca tcacgcttga taacgtcaag ctggtcagag tcgctccgct tatgcacgac 360  
atcaaggatc cttccagaga gaagcataac cacctggaac gtattgagtt ccgctacgag 420  
aaaatcacct ggacttacaa agacggcaac atcattcatt ccgactcgtg gaatgagcgt 480  
ccttccgcc 489

<210> 147 <211> 1650 <212> DNA <213> Escherichia coli <400> 147  
gtgaggaaca cgctgaaaca ggccatcgtg ctgtggggaa tgggtgttact gctgggtgctg 60  
tggtcagtgt ttatcagtcc gtctggcgtg ctgagatggg ccggtgcggc ggctatcgtt 120  
ctggcggttg ccgcgttggt gatttatcgg cgcaggcagg cgtggacgga gatgaccggc 180



gatgccgggt tgtcatcgct gccgccggaa acctaccgac agccggtagt gctgggtctgt 240  
 ggcgggtctgt cggcgccacct gtccactgac agcccgggtcc gccaggtttc agaagggtg 300  
 tatctgcatg ttctgatga agaacagctt gtggcgagcagg tggagcgatt gctgaccctt 360  
 cccccggcgt gggcatcgca gcttgccgtg gcgtatacca tcatgcccg catabaccgg 420  
 gatgtggcgg ttctggccgg acggctgcga cggttcgccc acagtatggc gacgggtgct 480  
 cgtcgggcag gcgtaaacgt cccctggctt ctctggagcg ggctgtccgg ctcccgcttg 540  
 ccggaaagag cgagttcacc gtggtttata tgtaccggcg gcgaagttca ggtagcaaca 600  
 tccacagaga ccaccatgcc cgcgcagtggt attgcacaat ccggcgtaga ggagcgcagt 660  
 cagcgactct gttacctgct gaaagctgaa agcctgatgc agtggctgaa tcttaatgtg 720  
 ctgacggcac tgaacggccc ggaggcgaaa tgtccaccac tggcgatgac cgtggggctg 780  
 gtccctcgt tgctgcgggt ggataacaac ctgtggcagt tgtggatcac cgccagaacc 840  
 ggctgacgc cggatatcgc ggacaccggc acagacgatg cgtgccatt cccggatgcc 900  
 ctgttacggc agttgcccg tcagtcgggc tttacccgc tgcgacgagc ctgctgacc 960  
 atgctgggcg tcaccaccgt ggcgggtatc gccgcgtgt gcctgtcagc cacggcaaatt 1020  
 cgccagttat tacggcaggt cggtgacgat ctgcaccgggt tttatgccgt cccgggtggag 1080  
 gaatttatca ccaaagcccg tcacctgtcg gtgctgaaag acgatgagc catgctcgat 1140  
 gggattacc gggaaggaga acccctgcgc ctccgtctgg ggttataccc cggcgaacgc 1200  
 atccgccagc cggattacg cgcattcgc gactggcgtc cgcctgaaca aaaaatggag 1260  
 gtgacggctt cgcttcaggt tcagaccgtg cgtcttgaca gtatgtcgt gtttgacgtc 1320  
 ggacaggccc gcctgaaaga cggctcgaca aaagtgtgtg tggacgcact ggtgaacatc 1380  
 cgggcaaaac cgggctggct gatcctcgtg gccggatata ccgatgccac cggcgatgaa 1440  
 aaaagcaatc agcagttatc gctgcggcgt gccgaagcgg tgcgcaactg gatgctgcag 1500  
 accagcgaca tcccggccac ctgttttgcc gtacaggggac tgggcgagag ccagcctgcg 1560  
 gcgaccaacg acacgccaca gggccgggca gtcaaccggc gtgtcgaaat cagtcttggt 1620  
 ccgcgttctg acgcctgtca ggacgtgaaa 1650

<210> 148 <211> 582 <212> DNA <213> Escherichia coli <400> 148  
 atgatcaaat ccacattctg gcgagcgctc gccctgaccg ctacgcttat cctcactggc 60  
 tntagccact cgcaaccgga acaggaaggc cggccgcagg cgtggctgca acctggtacg 120  
 ctcatcacgc tgctgcgcc ggggatttca cccgcagtca attcccagca actgttgacc 180  
 ggcagcttca acggcaaaac ccagtctctg ctagtgatgc ttaatgccga agatcagaaa 240  
 atcacccttg ccgggctgtc gtcggtcggc attcgccgtt ttctgggtgac ctacgatgca 300  
 aaagggttac gcgccgagca atccatcgtc gtcccacagt taccgcccgc aagtcaggta 360  
 ctggctgacg tgatgctcag ccactggccg attagcgctt ggcaaccgca acttcccaca 420

ggctggacgc ttcgcgacaa cggcgacaaa cgcgagctgc gtaacgccag cggcaaactg 480  
 gtcacggaaa tcacctatct gaatcgccag ggaaaacgcg tgccaatcag cattgagcag 540  
 catgtcttta aataccacat caccattcaa tacttaggtg ac 582

<210> 149 <211> 387 <212> DNA <213> Escherichia coli <400> 149  
 atgaaacgtt atataaaatg gtttgccatc acaattttta tcagtatgtt gaggcctgt 60  
 gtccgtacgg cccagtgca acagataagc accactgtca gtgtgggtca tactcaggag 120  
 cagggttaaaa atgccatttt gaaagcaggt gcgcagcgca agtggattat gacgcaagtg 180  
 tcccctggag ttattaaagc tcgctatcaa acacgaaatc acgttgcaga ggttcgtatt 240  
 acatatacag ctacctacta taacatcaaa tatgacagta gcctgaatct gcaggcttct 300  
 gatggaaaaa ttcataaaaa ctataaccgc tgggtgcgta acctggataa agatatacag 360  
 gttaacttat ctacaggagc aacgtta 387

<210> 150 <211> 1245 <212> DNA <213> Escherichia coli <400> 150  
 atgaagcgta aacatttgtt attattattg ttgttttcat tttccactaa cagtgcgcct 60  
 ctttactcct taattaggga ggcagttatg cagcatccca tagtaatgga agcccgggcg 120  
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Asp Thr Arg Gly Asp Thr Asn Trp Val Pro Pro Glu Gln Val Glu Arg  
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